

145891

STIC-Biotech/ChemLib

From: Bunner, Bridget  
Sent: Wednesday, February 23, 2005 9:28 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/056,583:

Please search the following short, related amino acid sequences:

1. SEQ ID NO: 65
2. SEQ ID NO: 86
3. SEQ ID NO: 89
4. SEQ ID NO: 90
5. SEQ ID NO: 93
6. SEQ ID NO: 97

Thanks!

Bridget Bunner

Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70

STIC  
FEB 23 2005  
10:00

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 76.6837 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-93  
Perfect score: 74  
Sequence: 1 EKPKEAVKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	5	ABP52299 HLA-DR2 m
2	69	93.2	15	5	ABP52291 HLA-DR2 m
3	69	93.2	15	5	ABP52297 HLA-DR2 m
4	68	91.9	15	5	ABP52305 HLA-DR2 m
5	64	86.5	15	5	ABP52300 HLA-DR2 m
6	63	85.1	15	5	ABP52290 HLA-DR2 m
7	63	85.1	15	5	ABP52292 HLA-DR2 m
8	63	85.1	15	5	ABP52304 HLA-DR2 m
9	61	82.4	17	5	ABP52303 HLA-DR2 m
10	58	78.4	781	8	ADN60395 B. lichen
11	58	78.4	781	8	ADN60505 B. lichen
12	58	78.4	781	8	ADN60519 B. lichen
13	57	77.0	17	5	ABP52302 HLA-DR2 m
14	53	71.6	15	5	ABP52271 HLA-DR2 m
15	53	71.6	15	5	ABP52289 HLA-DR2 m
16	53	71.6	15	5	ABP52298 HLA-DR2 m
17	53	71.6	17	5	ABP52294 HLA-DR2 m
18	53	71.6	17	5	ABP52296 HLA-DR2 m
19	53	71.6	19	5	ABP52295 HLA-DR2 m
20	49	66.2	15	5	ABP52293 HLA-DR2 m
21	49	66.2	15	5	ABP52301 HLA-DR2 m
22	48	64.9	299	4	ABP52276 Drosophila
23	48	64.9	299	8	ADP56704 Drosophila
24	47	63.5	15	5	ABP52270 HLA-DR2 m
25	47	63.5	15	5	ABP52272 HLA-DR2 m

26	44	59.5	362	3	AAg17822 Arabidops
27	44	59.5	364	3	AAg46637 Arabidops
28	44	59.5	461	3	AAg17821 Arabidops
29	44	59.5	462	3	AAg17820 Arabidops
30	44	59.5	463	3	AAg46636 Arabidops
31	44	59.5	464	3	AAg46635 Arabidops
32	44	59.5	572	4	ABP59072 Drosophila
33	43	58.1	15	5	ABP52263 HLA-DR2 m
34	43	58.1	428	8	ADP27881 Bacterial
35	42	56.8	306	4	AAU59347 Propionib
36	42	56.8	306	6	ABM55866 Propionib
37	42	56.8	312	2	AAW64153 Lettuce r
38	42	56.8	314	5	AAU95466 Lettuce p
39	42	56.8	444	4	ABG18307 Novel hum
40	42	56.8	774	4	ABG29304 Novel hum
41	42	56.8	791	8	ADQ26342 Chromobac
42	42	56.8	1402	2	AAW64150 Lettuce r
43	42	56.8	1402	5	AAU95463 Lettuce p
44	41	55.4	15	5	ABP52264 HLA-DR2 m
45	41	55.4	15	5	ABP52267 HLA-DR2 m

ALIGNMENTS

RESULT 1	ABP52299	ABP52299 standard; peptide; 15 AA.
ID	ABP52299	16-OCT-2002 (first entry)
XX	ABP52299;	HLA-DR2 molecule binding peptide SEQ ID NO:93.
AC	XX	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
DT	XX	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX	XX	immune response; antiinflammatory; neuroprotective; proliferation;
DE	XX	MHC class II protein inhibitor; demyelinating disease; inhibition;
XX	XX	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW	XX	anti-tumour necrosis factor agent.
OS	OS	Homo sapiens.
OS	OS	Synthetic.
PN	XX	WO200259143-A2.
XX	XX	01-AUG-2002.
PD	XX	24-JAN-2002; 2002MO-US002071.
XX	XX	24-JAN-2001; 2001US-0263569P.
PR	XX	(HARD ) HARVARD COLLEGE.
PA	XX	Strominger JL, Fridkis-Kareli M;
PI	XX	WPI; 2002-608439/65.
XX	XX	New compositions comprising synthetic peptides in complex with a major
PT	XX	histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT	XX	demyelinating disease, e.g. multiple sclerosis, or post-viral
PT	XX	encephalomyelitis.
PS	XX	Claim 28; Page 39; 54pp; English.
XX	XX	The present invention describes compositions (I) comprising a peptide
CC	CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	CC	residues. The complex of the peptide with a major histocompatibility
CC	CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	CC	comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
XX invention

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPA 15  
DB 1 EKPKVEAYKAAAPA 15

## RESULT 2

ABP52291 ID ABP52291 standard; peptide; 15 AA.

AC ABP52291;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:85.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

PS WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
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PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
XX invention

SQ Sequence 15 AA;

Query Match 93.2%; Score 69; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00013;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPA 15  
DB 1 EKPKVEAYKAAAPA 15

## RESULT 3

ABP52297 ID ABP52297 standard; peptide; 15 AA.

AC ABP52297;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:91.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

PS WPI; 2002-608439/65.

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PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

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CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
XX invention

SQ Sequence 15 AA;

Query Match 93.2%; Score 69; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00013;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPA 15

Db 1 EKPKVEAYKAAAPA 15

RESULT 4

ABP52305 standard; peptide; 15 AA.

AC ABP52305;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:99.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

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PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

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CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 15 AA;

Query Match 91.9%; Score 68; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00019;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15  
| | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | |  
Db 1 EKPKVEAYKAAAPA 15

RESULT 5  
ABP52300 standard; peptide; 15 AA.

XX ABP52300;  
AC 16-OCT-2002 (first entry)  
XX  
DT  
DE HLA-DR2 molecule binding peptide SEQ ID NO:94.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

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PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 15 AA;

Query Match 86.5%; Score 64; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.00089;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPA 15  
| | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | |  
Db 1 EKPKVEAFKAAAPA 15

RESULT 6  
ABP52290 standard; peptide; 15 AA.

AC ABP52290;  
DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:84.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX PS  
XX PT New compositions comprising synthetic peptides in complex with a major  
XX PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
XX PT encephalomyelitis.  
XX PS  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX CC residues. The complex of the peptide with a major histocompatibility  
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XX CC immune response. (I) has antiinflammatory and neuroprotective activities,  
XX CC and can be used as a MHC class II protein inhibitor. The compositions  
XX CC comprising the peptides are useful for treating demyelinating diseases  
XX CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine;  
XX CC demyelinating condition, and a side effect of administering an anti-  
XX CC tumour necrosis factor agents. The peptide further inhibits proliferation  
XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
XX CC ABP52305 represent peptides used in the exemplification of the present  
XX CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 85.1%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0013;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 7  
ABP52292  
ID ABP52292 standard; peptide; 15 AA.  
XX  
XX ABP52292;  
XX  
XX 16-OCT-2002 (first entry)  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:86.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX PS  
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XX CC residues. The complex of the peptide with a major histocompatibility  
XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
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XX CC tumour necrosis factor agents. The peptide further inhibits proliferation  
XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
XX CC ABP52305 represent peptides used in the exemplification of the present  
XX CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 85.1%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0013;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 8  
ABP52304  
ID ABP52304 standard; peptide; 15 AA.  
XX  
XX ABP52304;  
XX  
XX 16-OCT-2002 (first entry)  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:98.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200259143-A2.  
XX  
XX 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
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PA (HARD ) HARVARD COLLEGE.  
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PI Strominger JL, Fridkis-Hareli M;  
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DR WPI; 2002-608439/65.  
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PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
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CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
QY  
Query Match 85.1%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0013;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 1 EKPKEAYKAAAPA 15  
1 EAPKFEAYKAAAPA 15  
RESULT 9  
ABP52303  
ID ABP52303 standard; peptide; 17 AA.  
XX  
XX ABP52303;  
AC  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:97.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
PI Strominger JL, Fridkis-Hareli M;

XX  
DR WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
PS  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
QY  
Query Match 82.4%; Score 61; DB 5; Length 17;  
Best Local Similarity 86.7%; Pred. No. 0.0033;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 1 EKPKEAYKAAAPA 15  
3 EAPKFEAYKAAAPA 17  
RESULT 10  
ADN60395  
ID ADN60395 standard; protein; 781 AA.  
XX  
XX ADN60395;  
AC  
XX  
XX 01-JUL-2004 (first entry)  
DT  
XX  
XX B. licheniformis sporulation related polypeptide, seq id 67.  
DE  
XX  
XX Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;  
KW lyase; isomerase; ligase.  
KW  
XX  
XX Bacillus licheniformis.  
OS  
XX  
XX WO2003087148-A2.  
PN  
XX  
XX 23-OCT-2003.  
PD  
XX  
XX 25-MAR-2003; 2003WO-DK000200.  
PF  
XX  
XX 10-APR-2002; 2002DK-00000533.  
PR  
XX  
XX (NOVO ) NOVOZYMES AS.  
PA  
XX  
XX Andersen JT, Jorgensen ST, Raasmussen MD, Olsen PB, Clausen IG;  
PI  
XX  
XX WPI; 2004-122131/12.  
DR  
XX  
XX N-PSDB; ADN60394.  
DR  
XX  
XX A Bacillus licheniformis mutant host cell for producing a product of  
PT interest e.g. vitamins, antibiotics and enzymes.  
PT  
XX  
XX Claim 1; SEQ ID NO 67; 31pp; English.  
PS  
XX  
XX The invention relates to a Bacillus licheniformis mutant host cell  
CC derived from a parent B. licheniformis host cell. The mutant host cell is  
CC mutated in one or more genes encoding one or more polypeptides involved

CC in sporulation. The host cell comprises one or more heterologous genes  
CC present in at least two copies, encoding one or more heterologous  
CC polypeptides. The heterologous genes are stably integrated into the  
CC genome of the cell without leaving any antibiotic resistance marker genes  
CC at the site of integration. The heterologous genes are transcribed from a  
CC heterologous promoter or from an artificial promoter, and are comprised  
CC in an operon, preferably a polycistronic operon. The heterologous  
CC polypeptide is an antimicrobial peptide, or a fusion peptide comprising a  
CC peptide part which in its native form has antimicrobial activity. The  
CC heterologous polypeptide is an enzyme, preferably a secreted enzyme. The  
CC enzyme is an enzyme of a class selected from the group of enzyme classes  
CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC  
CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The *Bacillus*  
CC licheniformis is useful in a process for producing at least one product  
CC of interest, comprising cultivating a *B. licheniformis* mutant host cell  
CC in a suitable medium, whereby the said product is produced. The process  
CC further comprises isolating or purifying the product of interest. The  
CC current sequence represents a *B. licheniformis* sporulation related  
CC polypeptide.

CC Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;  
Best Local Similarity 73.3%; Pred. No. 0.53;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPPA 15  
|||:|:|:|:|  
Db 264 EKPEVQAYEAPAPPA 278

RESULT 11  
ADN60505

ID ADN60505 standard; protein; 781 AA.

AC ADN60505;

DT 01-JUL-2004 (first entry)

DE B. licheniformis sporulation related polypeptide, seq id 177.

XX Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;  
KW lyase; isomerase; ligase.

XX *Bacillus licheniformis*.

PN WO2003087148-A2.

PD 23-OCT-2003.

PF 25-MAR-2003; 2003WO-DK000200.

PR 10-APR-2002; 2002DK-00000533.

PA (NOVO ) NOVOZYMES AS.

PI Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PB, Clausen IG;

DR WPI; 2004-122131/12.

DR N-PSDB; ADN60504.

PT A *Bacillus licheniformis* mutant host cell for producing a product of  
PT interest e.g. vitamins, antibiotics and enzymes.

PS Claim 1; SEQ ID NO 177; 319pp; English.

XX The invention relates to a *Bacillus licheniformis* mutant host cell  
CC derived from a parent *B. licheniformis* host cell. The mutant host cell is  
CC mutated in one or more genes encoding one or more polypeptides involved  
CC in sporulation. The host cell comprises one or more heterologous genes  
CC present in at least two copies, encoding one or more heterologous  
CC polypeptides. The heterologous genes are stably integrated into the  
CC genome of the cell without leaving any antibiotic resistance marker genes

CC at the site of integration. The heterologous genes are transcribed from a  
CC heterologous promoter or from an artificial promoter, and are comprised  
CC in an operon, preferably a polycistronic operon. The heterologous  
CC polypeptide is an antimicrobial peptide, or a fusion peptide comprising a  
CC peptide part which in its native form has antimicrobial activity. The  
CC heterologous polypeptide is an enzyme, preferably a secreted enzyme. The  
CC enzyme is an enzyme of a class selected from the group of enzyme classes  
CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC  
CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The *Bacillus*  
CC licheniformis is useful in a process for producing at least one product  
CC of interest, comprising cultivating a *B. licheniformis* mutant host cell  
CC in a suitable medium, whereby the said product is produced. The process  
CC further comprises isolating or purifying the product of interest. The  
CC current sequence represents a *B. licheniformis* sporulation related  
CC polypeptide.

CC Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;  
Best Local Similarity 73.3%; Pred. No. 0.53;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPPA 15  
|||:|:|:|:|  
Db 264 EKPEVQAYEAPAPPA 278

RESULT 12  
ADN60519

ID ADN60519 standard; protein; 781 AA.

AC ADN60519;

DT 01-JUL-2004 (first entry)

DE B. licheniformis sporulation related polypeptide, seq id 191.

XX Mutant host cell; sporulation; oxidoreductase; transferase; hydrolase;  
KW lyase; isomerase; ligase.

XX *Bacillus licheniformis*.

PN WO2003087148-A2.

PD 23-OCT-2003.

PF 25-MAR-2003; 2003WO-DK000200.

PR 10-APR-2002; 2002DK-00000533.

PA (NOVO ) NOVOZYMES AS.

PI Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PB, Clausen IG;

DR WPI; 2004-122131/12.

DR N-PSDB; ADN60518.

PT A *Bacillus licheniformis* mutant host cell for producing a product of  
PT interest e.g. vitamins, antibiotics and enzymes.

PS Claim 1; SEQ ID NO 191; 319pp; English.

XX The invention relates to a *Bacillus licheniformis* mutant host cell  
CC derived from a parent *B. licheniformis* host cell. The mutant host cell is  
CC mutated in one or more genes encoding one or more polypeptides involved  
CC in sporulation. The host cell comprises one or more heterologous genes  
CC present in at least two copies, encoding one or more heterologous  
CC polypeptides. The heterologous genes are stably integrated into the  
CC genome of the cell without leaving any antibiotic resistance marker genes  
CC at the site of integration. The heterologous genes are transcribed from a  
CC heterologous promoter or from an artificial promoter, and are comprised  
CC in an operon, preferably a polycistronic operon. The heterologous  
CC polypeptide is an antimicrobial peptide, or a fusion peptide comprising a

CC peptide part which in its native form has antimicrobial activity. The  
CC heterologous polypeptide is an enzyme, preferably a secreted enzyme. The  
CC enzyme is an enzyme of a class selected from the group of enzyme classes  
CC consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC  
CC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). The Bacillus  
CC licheniformis is useful in a process for producing at least one product  
CC of interest, comprising cultivating a B. licheniformis mutant host cell  
CC in a suitable medium, whereby the said product is produced. The process  
CC further comprises isolating or purifying the product of interest. The  
CC current sequence represents a B. licheniformis sporulation related  
CC polypeptide.

XX  
SQ Sequence 781 AA;

Query Match 78.4%; Score 58; DB 8; Length 781;  
Best Local Similarity 73.3%; Pred. No. 0.53;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPA 15  
|||:|:|:|:|:|:|  
DB 264 EKPEVQAYEAPAPA 278

#### RESULT 13

ABP52302  
ID ABP52302 standard; peptide; 17 AA.

XX  
AC ABP52302;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:96.

XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX  
OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

XX  
PD 01-AUG-2002.

XX  
PF 24-JAN-2002; 2002WO-US002071.

XX  
PR 24-JAN-2001; 2001US-0263569P.

XX  
PA (HARD ) HARVARD COLLEGE.

XX  
PI Strominger JL, Fridkis-Hareli M;

XX  
DR WPI; 2002-608439/65.

XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX  
PS Claim 28; Page 39; 54pp; English.

XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX  
SQ Sequence 17 AA;

Query Match 77.0%; Score 57; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.015;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPA 15  
|||:|:|:|:|:|:|  
DB 3 EKAKFEAFKAAAPA 17

#### RESULT 14

ABP52271  
ID ABP52271 standard; peptide; 15 AA.

XX  
AC ABP52271;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX  
OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

XX  
PD 01-AUG-2002.

XX  
PF 24-JAN-2002; 2002WO-US002071.

XX  
PR 24-JAN-2001; 2001US-0263569P.

XX  
PA (HARD ) HARVARD COLLEGE.

XX  
PI Strominger JL, Fridkis-Hareli M;

XX  
DR WPI; 2002-608439/65.

XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX  
PS Claim 28; Page 39; 54pp; English.

XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX  
SQ Sequence 15 AA;

Query Match 71.6%; Score 53; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.064;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Search completed: February 26, 2005, 23:48:24  
Job time : 77.6837 secs

OY 1 EKPKVEAYKAAAPPA 15  
Db 1 EKAKVEAYKAAAAA 15

RESULT 15

ABP52289  
ID ABP52289 standard; peptide; 15 AA.

AC ABP52289;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:83.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-6b8439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

SQ Sequence 15 AA;

Query Match 71.6%; Score 53; DB 5; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.064;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAAPPA 15

Db 1 EAPAYKAYKAAAPPA 15

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 20.051 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-93  
Perfect score: 74  
Sequence: 1 EKPXVEAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	56.8	314	3 US-09-004-838-14	Sequence 14, Appl
2	42	56.8	1402	3 US-09-004-838-11	Sequence 11, Appl
3	41	55.4	297	4 US-09-252-991A-18932	Sequence 18932, A
4	40	54.1	75	4 US-09-513-999C-5101	Sequence 5101, Ap
5	40	54.1	222	4 US-09-949-016-9547	Sequence 9547, Ap
6	40	54.1	501	4 US-09-902-540-11248	Sequence 11248, A
7	39	52.7	76	4 US-09-270-767-61694	Sequence 61694, A
8	39	52.7	197	4 US-09-902-540-12825	Sequence 12825, A
9	39	52.7	435	4 US-09-949-016-7245	Sequence 7245, Ap
10	38.5	52.0	170	6 5215917-2	Patent No. 5215917
11	38.5	52.0	170	6 5472844-2	Patent No. 5472844
12	38.5	52.0	170	6 5215917-2	Patent No. 5215917
13	38.5	52.0	170	6 5472844-2	Patent No. 5472844
14	38	51.4	122	4 US-09-270-767-35661	Sequence 35661, A
15	38	51.4	122	4 US-09-270-767-50878	Sequence 50878, A
16	38	51.4	159	4 US-09-732-210-832	Sequence 832, App
17	38	51.4	208	4 US-09-902-540-16427	Sequence 16427, A
18	38	51.4	488	2 US-08-928-692-10	Sequence 10, Appl
19	38	51.4	488	2 US-09-339-972-10	Sequence 10, Appl
20	38	51.4	605	4 US-08-714-741-46	Sequence 46, Appl
21	38	51.4	642	4 US-09-489-039A-12434	Sequence 12434, A
22	38	51.4	1192	4 US-09-902-540-12662	Sequence 12662, A
23	37	50.0	72	4 US-09-621-976-3951	Sequence 3951, Ap
24	37	50.0	80	4 US-09-902-540-14758	Sequence 14758, A
25	37	50.0	132	3 US-09-724-864-65	Sequence 65, Appl
26	37	50.0	142	4 US-09-949-016-10395	Sequence 10395, A
27	37	50.0	155	4 US-09-732-210-836	Sequence 836, App

28	37	50.0	211	4 US-09-276-438-5	Sequence 5, Appl
29	37	50.0	251	4 US-09-902-540-14930	Sequence 14930, A
30	37	50.0	341	4 US-09-902-540-14167	Sequence 14167, A
31	37	50.0	861	4 US-09-949-016-10418	Sequence 10418, A
32	37	50.0	1387	4 US-09-902-540-11948	Sequence 11948, A
33	37	50.0	1431	4 US-09-902-540-10614	Sequence 10614, A
34	36.5	49.3	168	4 US-09-479-040-7	Sequence 7, Appl
35	36	48.6	60	1 US-08-346-849-16	Sequence 16, Appl
36	36	48.6	60	2 US-08-293-284A-16	Sequence 16, Appl
37	36	48.6	60	4 US-08-898-300-16	Sequence 16, Appl
38	36	48.6	60	4 US-08-824-513-16	Sequence 16, Appl
39	36	48.6	81	4 US-09-270-767-62451	Sequence 62451, A
40	36	48.6	125	4 US-09-770-834-11	Sequence 11, Appl
41	36	48.6	141	4 US-09-902-540-10465	Sequence 10465, A
42	36	48.6	193	4 US-09-252-991A-21712	Sequence 21712, A
43	36	48.6	290	4 US-09-358-383C-8	Sequence 8, Appl
44	36	48.6	340	4 US-09-543-681A-7850	Sequence 7850, Ap
45	36	48.6	351	4 US-09-809-665A-157	Sequence 157, App

ALIGNMENTS

RESULT 1  
US-09-004-838-14  
; Sequence 14, Application US/09004838  
; Patent No. 6350933  
; GENERAL INFORMATION:  
; APPLICANT: Michelmore, Richard W.  
; APPLICANT: Shen, Kathy  
; TITLE OF INVENTION: Procedures and Materials for  
; TITLE OF INVENTION: Confering Pest Resistance in Plants  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/004, 838  
; FILING DATE: 09-JAN-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/781,734  
; FILING DATE: 10-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einhorn, Gregory P.  
; REGISTRATION NUMBER: 38,440  
; REFERENCE/DOCKET NUMBER: 023070-078810US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..314  
; OTHER INFORMATION: /note= "RUGID amino acids"  
; US-09-004-838-14



; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9547  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9547

Query Match 54.1%; Score 40; DB 4; Length 222;  
Best Local Similarity 64.3%; Pred. No. 30;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAP 15  
Db 32 EPKKEAAKPAAP 45

## RESULT 6

US-09-902-540-11248  
; Sequence 11248, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 11248  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-11248

Query Match 54.1%; Score 40; DB 4; Length 501;  
Best Local Similarity 57.1%; Pred. No. 74;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKPVEAYKAAAP 14  
Db 258 ERPKVADLRVAAAP 271

## RESULT 7

US-09-270-767-61694  
; Sequence 61694, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 61694  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-61694

Query Match 52.7%; Score 39; DB 4; Length 76;  
Best Local Similarity 53.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAP 14  
Db 14 KPRTKXYRKAQTP 26

## RESULT 8

US-09-902-540-12825  
; Sequence 12825, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 12825  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-12825

Query Match 52.7%; Score 39; DB 4; Length 197;  
Best Local Similarity 60.0%; Pred. No. 39;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 EKPVEAYKAAAP 15  
Db 19 ESPAAEKPNAAAP 33

## RESULT 9

US-09-949-016-7245  
; Sequence 7245, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7245  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7245

Query Match 52.7%; Score 39; DB 4; Length 435;  
Best Local Similarity 46.7%; Pred. No. 94;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKPVEAYKAAAP 15  
Db 336 QPPALKAYPASTPA 350

## RESULT 10

US-09-949-016-7245

```
;Patent No. 5215917
; APPLICANT: DE ARAUJO, FAUSTO G.;PRINCE, JEFFREY B.;REMINGTON,
; JACK S.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING THE TOXOPLASMA
; GONDII P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5215917-2

Query Match      52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

OY      1 EKPKEAYKA---AAAPA 15
      |||:| |||
Db      99 EKPQVLCKVCVAEAGAPA 116

RESULT 11
5472844-2
;Patent No. 5472844
; APPLICANT: DE ARAUJO, FAUSTO G.;PRINCE, JEFFREY B.;
; REMINGTON JACK S.
; TITLE OF INVENTION: METHODS OF DETECTION OF TOXOPLASMA
; GONDII P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,540
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 24,932
; FILING DATE: 02-MAR-1993
; APPLICATION NUMBER: 431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5472844-2

Query Match      52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

OY      1 EKPKEAYKA---AAAPA 15
      |||:| |||
Db      99 EKPQVLCKVCVAEAGAPA 116

RESULT 12
5215917-2
;Patent No. 5215917
; APPLICANT: DE ARAUJO, FAUSTO G.;PRINCE, JEFFREY B.;REMINGTON,
; JACK S.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING THE TOXOPLASMA
; GONDII P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5215917-2

Query Match      52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;
```

```
RESULT 13
5472844-2
;Patent No. 5472844
; APPLICANT: DE ARAUJO, FAUSTO G.;PRINCE, JEFFREY B.;
; REMINGTON JACK S.
; TITLE OF INVENTION: METHODS OF DETECTION OF TOXOPLASMA
; GONDII P22 GENE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,540
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 24,932
; FILING DATE: 02-MAR-1993
; APPLICATION NUMBER: 431,669
; FILING DATE: 03-NOV-1989
; SEQ ID NO:2:
; LENGTH: 170
5472844-2

Query Match      52.0%; Score 38.5; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

OY      1 EKPKEAYKA---AAAPA 15
      |||:| |||
Db      99 EKPQVLCKVCVAEAGAPA 116

RESULT 14
US-09-270-767-35661
; Sequence 35661, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 35661
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35661

Query Match      51.4%; Score 38; DB 4; Length 122;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 EKPKEAYKAA 11
      ||| |||
Db      34 EKPKEVLSAA 44

RESULT 15
US-09-270-767-50878
; Sequence 50878, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 50878
```

```

; LENGTH: 122
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50878

```

```

Query Match      51.4%; Score 38; DB 4; Length 122;
Best Local Similarity 72.7%; Pred. NO. 35;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 EKPKEAYKAA 11
        |||||
Db      34 EKPKEVLAAA 44

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Job time : 21.051 secs

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GenCore version 5.1.6  
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OM protein - prdtein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 53.5714 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-93  
Perfect score: 74  
Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	US-10-056-583-93	Sequence 93, Appl
2	69	93.2	15	US-10-056-583-85	Sequence 85, Appl
3	69	93.2	15	US-10-056-583-91	Sequence 91, Appl
4	68	91.9	15	US-10-056-583-99	Sequence 99, Appl
5	64	86.5	15	US-10-056-583-94	Sequence 94, Appl
6	63	85.1	15	US-10-056-583-84	Sequence 84, Appl
7	63	85.1	15	US-10-056-583-86	Sequence 86, Appl
8	63	85.1	15	US-10-056-583-98	Sequence 98, Appl
9	61	82.4	17	US-10-056-583-97	Sequence 97, Appl
10	57	77.0	17	US-10-056-583-96	Sequence 96, Appl
11	53	71.6	15	US-10-056-583-65	Sequence 65, Appl
12	53	71.6	15	US-10-056-583-83	Sequence 83, Appl
13	53	71.6	17	US-10-056-583-88	Sequence 88, Appl

14	53	71.6	17	14	US-10-056-583-90	Sequence 90, Appl
15	53	71.6	19	14	US-10-056-583-89	Sequence 89, Appl
16	52	70.3	15	14	US-10-056-583-92	Sequence 92, Appl
17	49	66.2	15	14	US-10-056-583-87	Sequence 87, Appl
18	49	66.2	15	14	US-10-056-583-95	Sequence 95, Appl
19	47	63.5	15	14	US-10-056-583-64	Sequence 64, Appl
20	47	63.5	15	14	US-10-056-583-66	Sequence 66, Appl
21	45	60.8	444	16	US-10-437-963-162452	Sequence 162452, A
22	43	58.1	15	14	US-10-056-583-57	Sequence 57, Appl
23	43	58.1	265	15	US-10-424-599-180279	Sequence 180279, A
24	43	58.1	265	15	US-10-425-114-54748	Sequence 54748, A
25	43	58.1	428	15	US-10-369-493-16914	Sequence 16914, A
26	43	58.1	767	16	US-10-437-963-119955	Sequence 119955, A
27	42	56.8	264	15	US-10-424-599-162901	Sequence 162901, A
28	41	55.4	15	14	US-10-056-583-51	Sequence 51, Appl
29	41	55.4	15	14	US-10-056-583-53	Sequence 53, Appl
30	41	55.4	15	14	US-10-056-583-58	Sequence 58, Appl
31	41	55.4	15	14	US-10-056-583-61	Sequence 61, Appl
32	41	55.4	158	16	US-10-767-701-44713	Sequence 44713, A
33	41	55.4	193	15	US-10-613-728-6	Sequence 6, Appl
34	41	55.4	487	16	US-10-437-963-130505	Sequence 130505, A
35	40	54.1	15	9	US-09-765-301-19	Sequence 19, Appl
36	40	54.1	15	10	US-09-765-644A-19	Sequence 19, Appl
37	40	54.1	15	14	US-10-056-583-59	Sequence 59, Appl
38	40	54.1	15	15	US-10-438-538-23	Sequence 23, Appl
39	40	54.1	141	15	US-10-424-599-208066	Sequence 208066, A
40	40	54.1	157	16	US-10-437-963-169056	Sequence 169056, A
41	40	54.1	197	15	US-10-440-464-111	Sequence 111, App
42	40	54.1	238	15	US-10-425-114-69810	Sequence 69810, A
43	40	54.1	362	16	US-10-437-963-146726	Sequence 146726, A
44	40	54.1	401	15	US-10-369-493-15856	Sequence 15856, A
45	40	54.1	404	15	US-10-369-493-15485	Sequence 15485, A

ALIGNMENTS

RESULT 1  
US-10-056-583-93  
; Sequence 93, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-93

Query Match 100.0%; Score 74; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 15  
Db 1 EKPKEAYKAAAPA 15

```
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85.
```

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Query Match          93.2%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKEAYKAAAPAA 15
        |||||
Db       1 EKPKEAYKAAAPAA 15
```

```
RESULT 3
US-10-056-583-91.
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
```

```
Query Match          93.2%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKEAYKAAAPAA 15
        |||||
Db       1 EKPKEAYKAAAPAA 15
```

```
RESULT 4
US-10-056-583-99
; Sequence 99, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
```

```
Query Match          91.9%; Score 68; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.5e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKEAYKAAAPAA 15
        |||||
Db       1 EAPKEAYKAAAPAA 15
```

```
RESULT 5
US-10-056-583-94
; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94
```

```
Query Match          86.5%; Score 64; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00041;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKPKEAYKAAAPAA 15
        |||||
Db       1 EKPKEAYKAAAPAA 15
```

```
RESULT 6
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
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```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match      85.1%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0006;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPA 15
      ||| ||| ||| ||| |||
Db      1 EAPKYEAYKAAAPA 15

RESULT 7
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match      85.1%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0006;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPA 15
      ||| ||| ||| ||| |||
Db      1 EAPKYEAYKAAAPA 15

RESULT 8
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98
```

```
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98

Query Match      85.1%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0006;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPA 15
      ||| ||| ||| ||| |||
Db      1 EAPKFEAYKAAAPA 15

RESULT 9
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

Query Match      82.4%; Score 61; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPA 15
      ||| ||| ||| ||| |||
Db      3 EKAKFEAYKAAAPA 17

RESULT 10
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-96

Query Match 77.0%; Score 57; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0073;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
|||:|||||  
Db 3 EKAKFEAFKAAAPAA 17

RESULT 11

US-10-056-583-65  
; Sequence 65, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-65

Query Match 71.6%; Score 53; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.031;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
|||:|||||  
Db 1 EKAKYEAYKAAAAAA 15

RESULT 12

US-10-056-583-83  
; Sequence 83, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-83

Query Match 71.6%; Score 53; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.031;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
|||:|||||  
Db 1 EAPAYKAYKAAAPAA 15

RESULT 13

US-10-056-583-88  
; Sequence 88, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-88

Query Match 71.6%; Score 53; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.035;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
|||:|||||  
Db 3 EKAKYEAYKAAAAAA 17

RESULT 14

US-10-056-583-90  
; Sequence 90, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-90

Query Match 71.6%; Score 53; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.035;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
|||:|||||  
Db 1 EKAKYEAYKAAAAAA 15

## RESULT 15

US-10-056-583-89

; Sequence 89, Application US/10056583

; Publication No. US20030064915A1

; GENERAL INFORMATION:

; APPLICANT: Presidents and Fellows of Harvard College

; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/10/056,583

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 89

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-89

## Query Match

71.6%; Score 53; DB 14; Length 19;

Best Local Similarity 80.0%; Pred. No. 0.04;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKKAAPAA 15

DB 3 EKAKVEAYKKAAPAA 17

Search completed: February 27, 2005, 00:05:23  
Job time : 53.5714 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 13.3163 Seconds  
(without alignments)  
108.382 Million cell updates/sec

Title: US-10-056-583A-93  
Perfect score: 74  
Sequence: 1 EKPKEAYKAAAPPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	64.9	389	2 G87332	hypothetical prote
2	45	60.8	193	1 M0MS4B	myosin alkali ligh
3	45	60.8	306	2 G96014	hypothetical prote
4	45	60.8	765	2 T15447	hypothetical prote
5	43	58.1	50	2 G97151	hypothetical prote
6	43	58.1	270	2 T11225	traf protein homol
7	43	58.1	428	2 B87463	hypothetical prote
8	42	56.8	185	1 M0CH4E	myosin alkali ligh
9	42	56.8	193	1 M0RT4E	myosin alkali ligh
10	42	56.8	200	2 T48130	hypothetical prote
11	42	56.8	337	1 C70473	phosphate-binding
12	42	56.8	398	2 T21061	hypothetical prote
13	42	56.8	461	2 A13358	pyruvate dehydrog
14	42	56.8	656	2 A61479	probable cell surf
15	41	55.4	168	2 A45943	vitelline membrane
16	41	55.4	336	1 S75272	cytochrome d ubiq
17	41	55.4	810	2 C95401	probable oxidoredu
18	40	54.1	114	2 G81353	hypothetical prote
19	40	54.1	197	1 M0HU4E	myosin alkali ligh
20	40	54.1	300	2 H87631	integral membrane
21	40	54.1	452	2 T25076	hypothetical prote
22	40	54.1	586	2 T29657	hypothetical prote
23	40	54.1	729	2 T51896	probable translati
24	40	54.1	891	2 AC3384	ribonuclease E / z
25	39	52.7	145	2 T13550	hypothetical prote
26	39	52.7	179	2 F97683	50S ribosomal prot
27	39	52.7	179	2 AF2908	50S ribosomal prot
28	39	52.7	231	2 S18006	histone H1 - midge
29	39	52.7	379	2 T08277	carotenoid biosynt

30	39	52.7	508	2 S19266	anthranilate synth
31	39	52.7	594	1 D55514	dihydrolipoamide d
32	39	52.7	688	2 H96681	protein F1B22.10 l
33	39	52.7	723	2 AG3555	histidine ammonia-
34	38.5	52.0	186	2 A44968	surface antigen P2
35	38.5	52.0	447	2 AB3359	dihydrolipoamide S
36	38.5	52.0	762	2 H87302	chemotaxis protein
37	38	51.4	98	2 PU0034	photosystem I chai
38	38	51.4	160	2 JC2012	ribosomal protein
39	38	51.4	225	2 T05334	endomembrane-assoc
40	38	51.4	246	2 H71548	hypothetical prote
41	38	51.4	346	2 AH2308	cytochrome D ubiq
42	38	51.4	353	2 AB1823	hypothetical prote
43	38	51.4	546	2 T06415	calnexin - soybean
44	38	51.4	622	2 T29508	hypothetical prote
45	38	51.4	629	2 AH0521	dihydrolipoamide a

## ALIGNMENTS

```
RESULT 1
G87332
hypothetical protein CC0674 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87332
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: G87332
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-389 <STO>
A/Cross-references: UNIPROT:Q9NAC8; GB:AE005673; NID:q13421893; PIDN:AAK22659.1; GSPDB:
C/Genetics:
A/Gene: CC0674

Query Match          64.9%; Score 48; DB 2; Length 389;
Best Local Similarity 71.4%; Pred. No. 2.3;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      2 KPKVEAYKAAAPPA 15
          |||:|||||
Db      66 KTSVETFKAAAPPA 79

RESULT 2
M0MS4B
myosin alkali light chain 4, embryonic and atrial - mouse
N/Alternate names: MLC1A; MLC1emb; myosin I1 catalytic light chain, atrial
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A31114; S01944
R/Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Sassoon, D.; Weydert, A.; Buckingh
J. Biol. Chem. 263, 12669-12676, 1988
A/Title: Structure and sequence of the myosin alkali light chain gene expressed in adult
A/Reference number: A31114; MUID:88315068; PMID:2842339
A/Accession: A31114
A/Molecule type: DNA
A/Residues: 1-193 <BAR>
A/Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:q139731; PIDN:
R/Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
Nucleic Acids Res. 16, 10037-10052, 1988
A/Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striat
A/Reference number: S01944; MUID:89057447; PMID:3194193
A/Accession: S01944
A/Molecule type: DNA
A/Residues: 1-41 <COH>
A/Cross-references: EMBL:X12971; NID:g53138; PIDN:CAA31414.1; PID:g53139
```

C/Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fetal  
C/Genetics:  
A/Introns: 41/3; 51/1; 101/1; 159/1; 185/1  
C/Suprafamily: calmodulin; calmodulin repeat homology  
C/Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract  
F/47-81/Domain: calmodulin repeat homology <EF1>  
F/126-158/Domain: calmodulin repeat homology <EF3>  
F/161-193/Domain: calmodulin repeat homology <EF4>

Query Match 60.8%; Score 45; DB 1; Length 193;  
Best Local Similarity 71.4%; Pred. No. 3.7;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15  
Db 7 EPKKEAKPAAAPA 20

## RESULT 3

G96014

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymb

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C/Accession: G96014

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo

A/Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: G96014

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-306 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q92TW2; GB:AL591985; PIDN:CAC49783.1; PID:g15141270; GSPDB:C

A/Experimental source: strain 1021, megaplasmid pSymb

R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: SMD20676

A/Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 306;  
Best Local Similarity 57.1%; Pred. No. 5.8;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15

Db 66 RPQPEAFPSAAAPA 79

## RESULT 4

T15447

hypothetical protein C07G1.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T15447

R/Hawkins, J.

submitted to the EMBL Data Library, May 1996

A/Description: The sequence of C. elegans cosmid C07G1.

A/Reference number: Z18352

A/Accession: T15447

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-765 &lt;HAW&gt;

A/Cross-references: UNIPROT:Q17796; EMBL:U58751; NID:g1326379; PID:g1326382; PIDN:AAB006

A/Experimental source: strain Bristol N2, clone C07G1

C/Genetics:

A/Gene: CESP:C07G1.5  
A/Map position: 4  
A/Introns: 33/3; 46/1; 74/2; 136/3; 554/3; 681/1; 742/1

Query Match 60.8%; Score 45; DB 2; Length 765;  
Best Local Similarity 61.5%; Pred. No. 14;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAP 14  
Db 326 KPEVDGYKGAAP 338

## RESULT 5

G97151

hypothetical protein CAC2043 [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C/Accession: G97151

R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: G97151

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-50 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q97HG8; GB:AE001437; PIDN:AAK80002.1; PID:g15025028; GSPDB:C

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC2043

Query Match 58.1%; Score 43; DB 2; Length 50;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKPKVEAYK 9  
Db 35 EKPKVEAYK 43

## RESULT 6

T31225

traf protein homolog - Sphingomonas aromaticivorans plasmid pNL1

C/Species: Sphingomonas aromaticivorans

C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T31225

R/Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.;

submitted to the EMBL Data Library, July 1998

A/Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati

A/Reference number: Z20992

A/Accession: T31225

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-270 &lt;ROM&gt;

A/Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:g3378261; PID:g3378366; PIDN:AAD0

C/Genetics:

A/Genome: plasmid pNL1

A/Note: traf

Query Match 58.1%; Score 43; DB 2; Length 270;  
Best Local Similarity 76.9%; Pred. No. 11;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKPKVEAYKAAA 13  
Db 54 EKPKVEAYKAAA 66

## RESULT 7

E87463

hypothetical protein CCI1729 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: E87463  
R;Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: E87463  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-428 <STO>  
A;Cross-references: UNIPROT:Q9A7J4; GB:AE005673; NID:g13423147; PIDN:AAK23705.1; GSPDB:C  
C;Genetics:  
A;Gene: CC1729  
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match	58.1%;	Score 43;	DB 2;	Length 428;
Best Local Similarity	90.9%;	Pred. No. 17;		
Matches 10;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 3 PKVEAYKAAA 13  
|||||  
Db 88 PKVEAPKAAA 98

## RESULT 8

myosin alkali light chain 4, embryonic - chicken  
 N:Alternate names: myosin I23 catalytic light chain  
 C:Species: Gallus gallus (chicken)  
 C:Date: 01-Dec-1989 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: S02065; A29473  
 R:Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriyama, Y.  
 J. Mol. Biol. 204, 497-505, 1988  
 A:Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic g  
 A:Reference number: S02065; MUID:89141751; PMID:3225843  
 A:Accession: S02065  
 A:Molecule type: DNA  
 A:Residues: 1-185 <NAB>  
 A:Cross-references: UNIPROT:P09540; EMBL:X14428  
 A:Note: the authors translated the codon CGG for residue 71 as Ala  
 R:Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.  
 J. Biol. Chem. 262, 14408-14414, 1987  
 A:Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac  
 A:Reference number: A29473; MUID:88032983; PMID:3667580  
 A:Accession: A29473  
 A:Molecule type: mRNA  
 A:Residues: 1-93, 'L', 95-165, 'L', 167-185 <KAW>  
 A:Cross-references: GB:J02823; NID:G212339; PIDN:AAA48957.1; PID:G212340  
 A:Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1  
 C:Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac  
 C:Genetics:  
 A:Introns: 33/3; 43/1; 93/1; 151/1; 177/1  
 C:Complex: The myosin molecule contains two heavy chains, two alkali light chains, and t  
 C:Superfamily: calmodulin; calmodulin repeat homology  
 C:Keywords: brain; calcium binding; duplication; EF hand; muscle contraction  
 F:39-73/Domain: calmodulin repeat homology <EF1>  
 F:118-150/Domain: calmodulin repeat homology <EF3>  
 F:153-185/Domain: calmodulin repeat homology <EF4>

Query Match	56.8%	Score 42;	DB 1;	Length 185;
Best local	Similarity 75.0%;	Pred. No. 11;		
Matches	9;	Conservative 1;	Mismatches 2;	Indels 0;
				Gaps 0;
QY	3 PKVEAYKAAAP	14		
	:			
Db	8 PKDDAAKAAAP	19		

RESULT 5  
MORT4E

myosin alkali light chain 4, embryonic and atrial - rat  
 N;Alternate names: MLC1A; MLClemb; myosin I1 catalytic light chain, atrial  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 29-Jan-1993 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
 C;Accession: S09236  
 R;Rovner, A.S.; McNally, E.M.; Leinwand, L.A.  
 Nucleic Acids Res. 18, 1581-1586, 1990  
 A;Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of express  
 A;Reference number: S09236; MUID:90221887; PMID:2326197  
 A;Accession: S09236  
 A;molecule type: mRNA  
 A;Residues: 1-193 <ROV>  
 A;Cross-references: UNIPROT:P17209; EMBL:X51531; NID:g57512; PIDN:CAA35911.1; PID:g5751  
 C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fe  
 C;Superfamily: calmodulin; calmodulin repeat homology  
 C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contra  
 F;47-81/Domain: calmodulin repeat homology <EF1>  
 F;126-158/Domain: calmodulin repeat homology <EF3>  
 F;161-193/Domain: calmodulin repeat homology <EF4>

Query Match	56.8%;	Score 42;	DB 1;	Length 193;
Best Local Similarity	64.3%;	Pred. No. 12;		
Matches	9;	Conservative	1;	Mismatches 4; Indels 0; Gaps 0;
QY	2	KPKVEAYKAAAPA	15	
	:			
Db	7	EPKKEATAKVAAAPA	20	

## RESULT 10

Query Match	56.8%;	Score 42;	DB 2;	Length 200;
Best Local Similarity	69.2%;	Pred. No. 12;		
Matches	9;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	1	EKPKEAYKAAA	13	
Db	180	EKPKEHAYKQEA	192	

## RESULT 11

phosphate-binding periplasmic protein - *Aquifex aeolicus*  
C/Species: *Aquifex aeolicus*  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: C70473  
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Co  
V.

Nature 392, 353-358, 1998  
A/Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A/Reference number: A70300; MUID:98196666; PMID:9537320  
A/Accession: C70473  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-337 <AQF>

A;Cross-references: UNIPROT:O67815; GB:AE000768; NID:g2984249; PIDN:AAC07783.1; PID:g298  
A;Experimental source: strain VFS  
C;Genetics:  
A;Gene: pats  
C;Superfamily: phosphate-repressible phosphate-binding protein

Query Match 56.8%; Score 42; DB 1; Length 337;  
Best Local Similarity 57.1%; Pred. No. 20;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15  
||:|||||  
Db 239 KPSIETFOAAANA 252

RESULT 12  
T21061  
hypothetical protein F17C11.9 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T21061

R;McMurray, A.

submitted to the EMBL Data Library, May 1996  
A;Reference number: Z19366

A;Accession: T21061

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-398 <WIL>

A;Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDN:CAA96631.1; GSPDB:GN00023; CESP:F1

A;Experimental source: clone F17C11

C;Genetics:

A;Gene: CESP:F17C11.9

A;Map position: 5

A;Introns: 3/3; 44/3; 151/3; 196/1; 354/3

C;Superfamily: translation elongation factor eEF-1 gamma chain

Query Match 56.8%; Score 42; DB 2; Length 398;  
Best Local Similarity 76.9%; Pred. No. 23;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKPKEAYKAAA 13  
|||||  
Db 214 EKPKEAKPAAA 226

RESULT 13

A13358

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) [imported] - *Brucella melitensis* (strain

C;Species: *Brucella melitensis*

C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 12-Jul-2004

C;Accession: A13358

R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A;Reference number: AD3252; PMID:11756688

A;Accession: A13358

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-461 <KUR>

A;Cross-references: UNIPROT:Q8YHE6; GB:AE008917; PIDN:AAL52036.1; PID:g17982802; GSPDB:G

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI0855

A;Map position: 1

C;Superfamily: pyruvate dehydrogenase complex, E1 component, beta subunit

C;Keywords: oxidoreductase

Query Match 56.8%; Score 42; DB 2; Length 461;  
Best Local Similarity 60.0%; Pred. No. 27;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKPKEAYKAAAPA 15

Db 100 EEPKAENKADAVPA 114  
||:|||||

RESULT 14

AE1479

probable cell surface protein (LPXTG motif) [imported] - *Listeria innocua* (strain Clp11

C;Species: *Listeria innocua*

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AE1479

R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshih, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schlueter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,

A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; NUID:21537279; PMID:11679669

A;Accession: AE1479

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-656 <GLA>

A;Cross-references: UNIPROT:Q92ET6; GB:A1592022; PIDN:CAC95605.1; PID:g16412801; GSPDB:G

A;Experimental source: strain Clp11262

C;Genetics:

A;Gene: lin0372

Query Match 56.8%; Score 42; DB 2; Length 656;  
Best Local Similarity 66.7%; Pred. No. 38;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 KVEAYKAAAPA 15  
||:|||||  
Db 26 KIDAVYAAAPA 37

RESULT 15

A45943

vitelline membrane protein 26A-4 precursor - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004

C;Accession: A45943

R;Popodi, E.; Minoo, P.; Burke, T.; Waring, G.L.

Dev. Biol. 127, 248-256, 1988

A;Title: Organization and expression of a second chromosome follicle cell gene cluster

A;Reference number: A45943; NUID:88242923; PMID:3132408

A;Accession: A45943

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-168 <POP>

A;Cross-references: UNIPROT:P13238; GB:M20936; NID:g158728; PID:g158729

C;Genetics:

A;Gene: FlyBase:Vn26Ab

A;Cross-references: FlyBase:FBgn0003980

Query Match 55.4%; Score 41; DB 2; Length 168;  
Best Local Similarity 61.5%; Pred. No. 15;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 PKVEAYKAAAPA 15  
||:|||||  
Db 67 PAAQAYSAPAPA 79

Search completed: February 26, 2005, 23:57:17  
Job time : 14.3163 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 65.2041 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-93  
Perfect score: 74  
Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	78.4	781	2	Q65JG3 bacillus 11
2	48	64.9	299	1	P50887 drosophila
3	48	64.9	312	2	Q9UANI drosophila
4	48	64.9	389	2	Q9AAC8 caulobacter
5	47	63.5	458	2	Q7SDS7 neurospora
6	46	62.2	555	2	Q7NVT5 chromobacter
7	46	62.2	1923	2	Q7S9W8 neurospora
8	45	60.8	192	1	MIEF_MOUSE
9	45	60.8	299	2	Q6YSU4 oryza sativ
10	45	60.8	306	2	Q92TW2 rhizobium m
11	45	60.8	439	2	Q869Y7 dictyosteli
12	45	60.8	729	2	Q17796 caenorhabdi
13	44	59.5	238	1	SSB_SHEON
14	44	59.5	342	2	Q62L76 burkholderi
15	44	59.5	342	2	Q63V82 burkholderi
16	44	59.5	447	2	Q8X0Q2 neurospora
17	44	59.5	462	2	Q9ZRO1 arabidopsis
18	44	59.5	464	2	Q9FLQ4 arabidopsis
19	44	59.5	574	2	Q8SXM8 drosophila
20	44	59.5	607	2	Q9W327 drosophila
21	43	58.1	50	2	Q97HG8 clostridium
22	43	58.1	136	2	Q8FR15 corynebacte
23	43	58.1	143	2	Q8KG95 chlorobium
24	43	58.1	227	2	Q95XQ6 caenorhabdi
25	43	58.1	270	2	Q85933 sphingomona
26	43	58.1	280	2	Q8U3Y4 pyrococcus
27	43	58.1	428	2	Q9A7J4 caulobacter
28	43	58.1	613	2	Q8RYZ1 oryza sativ
29	42.5	57.4	214	2	Q88LD7 pseudomonas
30	42	56.8	121	2	Q89NE4 bradyrhizob
31	42	56.8	163	2	Q6JRS4 equus caball

32	42	56.8	185	1	MIEF_CHICK	P09540 gallus gall
33	42	56.8	192	1	MIEF_RAT	P17209 rattus norv
34	42	56.8	200	2	Q9STU1	Q98TJ1 arabidopsis
35	42	56.8	249	2	Q892F2	Q892F2 clostridium
36	42	56.8	283	2	Q6A7J7	Q6A7J7 propionibac
37	42	56.8	337	2	Q67815	Q67815 aquifex aeo
38	42	56.8	359	2	Q6C8W3	Q6C8W3 yarrowia li
39	42	56.8	365	2	Q8BG01	Q8B901 m mus muscu
40	42	56.8	373	2	Q814K9	Q814K9 caenorhabdi
41	42	56.8	398	1	EPIG_CAEEL	P54412 caenorhabdi
42	42	56.8	437	1	FLHF_PSEPU	O52256 pseudomonas
43	42	56.8	461	2	Q8YHE6	O8YHE6 brucella me
44	42	56.8	461	2	Q8G0G7	Q8G0G7 brucella su
45	42	56.8	629	2	Q9DEI6	Q9DEI6 oreochromis

ALIGNMENTS

RESULT 1					
ID	Q65JG3	PRELIMINARY;	PRT;	781 AA.	
AC	Q65JG3;				
DT	25-OCT-2004 (TREMBlrel. 28, Created)				
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)				
DE	SpotIIE (DNA translocase).				
GN	Name=spotIIE; ORFNames=BL01204, BLi01906;				
OS	Bacillus licheniformis DSM 13.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=279010;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=DSM 13;				
RX	PubMed=15383718;				
RA	Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,				
RA	Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,				
RA	Ehrenreich A., Gottschalk G.;				
RT	"The Complete Genome Sequence of Bacillus licheniformis DSM13, an				
RT	Organism with Great Industrial Potential.";				
RL	J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 14580;				
RA	Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,				
RA	Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,				
RA	Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,				
RA	Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,				
RA	Berka R.M.;				
RT	"Complete genome sequence of the industrial bacterium Bacillus				
RT	licheniformis and comparisons with closely related Bacillus species.";				
RL	Genome Biol. 5:R77-R77 (2004).				
DR	EMBL; AE017333; AAU40801.1; -.				
DR	EMBL; CP000002; AAU23441.1; -.				
SQ	SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;				
Query Match					
		78.4%;	Score 58;	DB 2;	Length 781;
		Best Local Similarity 73.3%;	Pred. No. 0.51;		
		Matches 11;	Conservative 3;	Mismatches 1;	Indels 0;
				Gaps	0;
QY	1 EKPKEAYKAAAPA 15				
DB	264 EKPEVQAYEAPAPA 278				
RESULT 2					
RL22_DROME	STANDARD;	PRT;	299 AA.		
ID	RL22_DROME				
AC	P50887; Q9V3X9;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	25-JAN-2005 (Rel. 46, Last annotation update)				
DE	60S ribosomal protein L22.				

GN Name=Rpl22; ORFNames=CG7434;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Glover C.V.C., Bidwai A.P., Zhao W.F.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Spradling A.C., Stapleton M., Strong R., Smith T.,  
 RA Spieler E., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP GENOME REANNOTATION.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;  
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,  
 RA Dreano S., Gloux S., LeJaure V., Mottier S., Galibert F., Borkova D.,  
 RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,  
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,  
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,  
 RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,  
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
 RA Glover D.M.;  
 RT "From sequence to chromosome: the tip of the X chromosome of D.  
 RT melanogaster.";  
 RL Science 287:2220-2222(2000).  
 CC -1- SIMILARITY: Belongs to the ribosomal protein L22e family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U42587; AAB17433.1; -;  
 DR EMBL; AE003418; AAF45546.1; -;  
 DR EMBL; AL132792; CAB60023.1; -;  
 DR Intact; P50887; -;  
 DR FlyBase; FBgn0015288; Rpl22.  
 DR InterPro; IPR002671; Ribosomal\_L22e.  
 DR Pfam; PF01776; Ribosomal\_L22e; 1.  
 DR ProDom; PD007306; Ribosomal\_L22e; 1.  
 KW Ribosomal protein.  
 FT DOMAIN 24 31 Poly-Ala.  
 FT DOMAIN 46 50 Poly-Ala.  
 FT DOMAIN 65 70 Poly-Ala.  
 FT DOMAIN 93 98 Poly-Ala.  
 FT DOMAIN 103 112 Poly-Ala.  
 FT DOMAIN 136 152 Poly-Ala.  
 FT DOMAIN 185 188 Poly-Lys.  
 FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).  
 SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;  
 QY 1 EKPYEAYKAAAPA 15  
 Db 36 EKPYEAYKAAAPA 50  
 QY 36 EKPYEAYKAAAPA 50  
 ID Q9UANI PRELIMINARY; PRT; 312 AA.  
 AC Q9UANI;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ribosomal protein L22 (Fragment).  
 GN Name=Rpl22; Synonyms=rpl22;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;  
 RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;  
 RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal  
 RT proteins, L22 and L23a, with unique histone-like amino-terminal  
 RT extensions.";  
 RL Gene 226:339-345(1999).  
 DR EMBL; AF080131; AAD19341.1; -;  
 DR FlyBase; FBgn0015288; Rpl22.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.

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DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT NON_TER
SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;

Query Match 64.9%; Score 48; DB 2; Length 312;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPAA 15
Db 49 EKPKAEAAKPAAPAAA 63

RESULT 4
ID Q9AAC8 PRELIMINARY; PRT; 389 AA.
AC Q9AAC8;
DT 01-JUN-2003 (TREMBlrel. 17, Created)
DT 01-JUN-2003 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein CC0674.
GN OrderedLocusNames=CC0674;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteriaceae; Caulobacter.
OX NCBI_TaxID:155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton M.C., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL; AE005743; AAK22659.1; -.
DR PIR; G87332; G87332.
DR TIGR; CC0674; -.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000897; SRP54.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 389 AA; 40769 MW; C6DD05B8CE8D150E CRC64;

Query Match 64.9%; Score 48; DB 2; Length 389;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPAA 15
Db 66 KTSVETPKAAAPAA 79

RESULT 5
ID Q7SDS7 PRELIMINARY; PRT; 458 AA.
AC Q7SDS7;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU03083.1;
OS Neurospora crassa.

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass I., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mammaupt G., Ebdole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000044; EAA34940.1; -.
SQ SEQUENCE 458 AA; 49949 MW; 196D609BF9320496 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 458;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKVEAYKAAAPAA 15
Db 78 QPKPKQAAKAPAA 92

RESULT 6
ID Q7NVT5 PRELIMINARY; PRT; 555 AA.
AC Q7NVT5;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CV2257;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chneire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrazi L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Weisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,

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RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,  
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seanez H.N.,  
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,  
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,  
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Umenyi T.,  
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;  
 RT "The complete genome sequence of Chromobacterium violaceum reveals  
 RT remarkable and exploitable bacterial adaptability.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
 DR EMBL; AE016918; AAQ59929.1;  
 DR InterPro; IPR005475; Transketolase\_CR.  
 DR InterPro; IPR005474; Transketolase\_N.  
 DR InterPro; IPR009014; Transketolase\_C\_like.  
 DR Pfam; PF00456; Transketolase\_N; 1.  
 DR Pfam; PF02779; Transketolase\_N; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 555 AA; 60134 MW; AD11DEC79CA3EE01 CRC64;

Query Match 62.2%; Score 46; DB 2; Length 555;  
 Best Local Similarity 57.1%; Pred. No. 39;  
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPVEAYKAAAP 14  
 Db 526 EMPRIETFOAAAAP 539

RESULT 7  
 ID Q7S9W8 PRELIMINARY; PRT; 1923 AA.  
 AC Q7S9W8;  
 DT 01-MAR-2004 (TRENBLrel. 26, Created)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=NCU06338.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OR74A;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 RA Selltremlkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,  
 RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,  
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;  
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";  
 RT Nature 0:0-0(2003).  
 RL  
 CC -1- FUNCTION: Control of topological states of DNA by transient  
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II  
 CC makes double-strand breaks (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both  
 CC negative and positive supercoils, whereas prokaryotic enzymes  
 CC relax only negative supercoils (By similarity).  
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABX01000209; EAA33136.1; -.

DR HSP; P06786; IBJT.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.  
 DR GO; GO:0006265; P:DNA topological change; IEA.  
 DR InterPro; IPR003594; ATPbind\_ATPase.  
 DR InterPro; IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro; IPR011558; DNA\_gyrase\_B.  
 DR InterPro; IPR01241; DNA\_topoisom.  
 DR InterPro; IPR002205; DNA\_topoisom.  
 DR Pfam; PF00204; DNA\_gyraseB; 1.  
 DR Pfam; PF00521; DNA\_topoisom; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR PRINTS; PR00615; CCAATSUBUNTA.  
 DR PRINTS; PR00418; TP12FAMILY.  
 DR ProDom; PD149633; DNA\_gyrase\_B; 1.  
 DR ProDom; PD000742; DNA\_topoisom; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; UNKNOWN\_1.  
 KW ATP-binding; DNA-binding; Hypothetical protein; Isomerase;  
 KW Topoisomerase.  
 SQ SEQUENCE 1923 AA; 213143 MW; 10663EA61ED142E0 CRC64;

Query Match 62.2%; Score 46; DB 2; Length 1923;  
 Best Local Similarity 78.6%; Pred. No. 1.2e+02;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKVEAYKAAAPA 15  
 Db 1799 KPKVTAKKAAAAAA 1812

RESULT 8  
 ID MLEF\_MOUSE STANDARD; PRT; 192 AA.  
 AC P09541;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Myosin light chain 1, atrial/fetal isoform (MLC1A) (MLC1EMB).  
 GN Name=MLC1a; Synonyms=My1a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H;  
 RA MEDLINE=88315068; PubMed=2842339;  
 RA Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,  
 RA Buckingham M.E.;  
 RA "Structure and sequence of the myosin alkali light chain gene  
 RA expressed in adult cardiac atria and fetal striated muscle.";  
 RL J. Biol. Chem. 263:12669-12676(1988).  
 RN [2]  
 RP SEQUENCE OF 1-40 FROM N.A.  
 RC STRAIN=C3H;  
 RX MEDLINE=89057447; PubMed=3194193;  
 RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,  
 RA Buckingham M.E.;  
 RA "Promoter analysis of myosin alkali light chain genes expressed in  
 RA mouse striated muscle.";  
 RL Nucleic Acids Res. 16:10037-10052(1988).  
 CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light  
 CC chains.  
 CC -1- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal  
 CC skeletal and ventricular muscle.  
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS  
 CC PROTEIN DOES NOT BIND CALCIUM.  
 CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M20772; AAA39721.1; -  
DR EMBL; M31017; AAA39721.1; JOINED.  
DR EMBL; M20769; AAA39721.1; JOINED.  
DR EMBL; M20770; AAA39721.1; JOINED.  
DR EMBL; M20771; AAA39721.1; JOINED.  
DR EMBL; M12971; CAA31414.1; -  
DR EMBL; M19436; AAA39720.1; -  
DR PIR; A31114; MOMS4E.  
DR HSSP; P02607; 1BR1.  
DR MGD; MGI:97267; Myla.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_Like.  
DR ProDom; PD000012; EF-hand; 2.  
KW Multigene family; Muscle protein; Myosin.  
FT INIT\_MET 0  
SQ SEQUENCE 192 AA; 21028 MW; B0439D512FA19C38 CRC64;

Query Match 60.8%; Score 45; DB 1; Length 192;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15  
:|:|:|:|:|:|  
Db 6 EPKKEAAKPAAPA 19

## RESULT 9

O6YSU4 PRELIMINARY; PRT; 299 AA.  
AC Q6YSU4;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE Hypothetical protein P0680C01.22.  
GN Name=P0680C01.22;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
clone: P0680C01."  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP006344; BAC84796.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 299 AA; 31850 MW; 4C14C4070BC31552 CRC64;

Query Match 60.8%; Score 45; DB 2; Length 299;  
Best Local Similarity 73.3%; Pred. No. 33;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKPKEAYKAAAPA 15  
|:|:|:|:|:|  
Db 262 EAPKVEATPAAPAATA 276

## RESULT 10

O92TW2 PRELIMINARY; PRT; 306 AA.  
AC O92TW2;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hypothetical protein Smb20676.  
GN ORFNames=Smb20676;  
OS Rhizobium meliloti (Sinorhizobium meliloti).

OC plasmid pSymB.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;  
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,  
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,  
RA Golding B., Puehler A.;  
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-  
fixing endosymbiont Sinorhizobium meliloti."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).  
DR EMBL; AL591985; CAC49783.1; -  
DR PIR; G96014; G96014.  
DR InterPro; IPR009273; DUF930.  
DR Pfam; PF06059; DUF930; 1.  
KW Complete proteome; Hypothetical protein; Plasmid.  
SQ SEQUENCE 306 AA; 32638 MW; 01D9CC644001E67E CRC64;

Query Match 60.8%; Score 45; DB 2; Length 306;  
Best Local Similarity 57.1%; Pred. No. 34;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 KPKVEAYKAAAPA 15  
:|:|:|:|:|:|  
Db 66 RPQPEAFESAAPA 79

## RESULT 11

O869Y7 PRELIMINARY; PRT; 439 AA.  
AC Q869Y7;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Similar to Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
DE dihydrolipoamide succinyltransferase component of 2-oxoglutarate  
dehydrogenase complex, mitochondrial (EC 2.3.1.61) (E2) (E2K).  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;  
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,  
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."  
RL Nature 418:79-85(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RA Baumgart C.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
DR EMBL; AC116305; MA052267.1; -  
DR HSSP; P07016; 1C4T.  
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0004149; F:dihydrolipoalysine-residue succinyltransferase. .; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
DR InterPro; IPR001078; 2Oxoacid\_dh.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR01053; Hybrid\_motif.  
DR InterPro; IPR003016; Lipoyl\_BS.  
DR InterPro; IPR006255; SucB.  
DR Pfam; PF00198; 2-oxoacid\_dh; 1.

DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR ProDom; PD00115; 20xacid\_dh; 1.  
 DR TIGRFAMs; TIGR01347; sucb; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 KW Acyltransferase; Lipoyl; Transferase.  
 SQ SEQUENCE 439 AA; 47633 MW; 214DE063A7139A79 CRC64;

Query Match  
 Best Local Similarity 60.8%; Score 45; DB 2; Length 439;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 PKVEAYKAAAP 14  
 |||||  
 DB 156 PKVEAPKAAEAP 167

RESULT 12  
 Q17796 PRELIMINARY; PRT; 729 AA.

ID Q17796  
 AC Q17796;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Prion-like (Q/n-rich)-domain-bearing protein protein 9.  
 GN Name=pqn-9; ORFNames=C07G1.5;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG WormBase Consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Hawkins J.;  
 RT "The sequence of C. elegans cosmid C07G1.";  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilson R.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RG WormBase Consortium;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U58751; AAB00658.2; -  
 DR PIR; T15447; T15447.  
 DR HSSP; Q960X8; 1DVP.  
 DR IntAct; Q17796; -  
 DR WormBase; WBGene0004101; pqn-9.  
 DR WormPep; C07G1.5; CE32574.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006886; P:intracellular protein transport; IEA.  
 DR InterPro; IPR008942; ENTH\_VHS.  
 DR InterPro; IPR011011; FYVE\_PHD\_Znf.  
 DR InterPro; IPR003903; UIM.  
 DR InterPro; IPR002014; VHS.  
 DR InterPro; IPR000306; Znf\_FYVE.  
 DR Pfam; PF01363; FYVE; 1.  
 DR Pfam; PF02809; UIM; 1.

DR Pfam; PF00790; VHS; 1.  
 DR SMART; SM00064; FYVE; 1.  
 DR SMART; SM00726; UIM; 1.  
 DR SMART; SM00288; VHS; 1.  
 DR PROSITE; PS50330; UIM; 1.  
 DR PROSITE; PS50179; VHS; 1.  
 DR PROSITE; PS50178; ZF\_FYVE; 1.  
 KW Prion.  
 SQ SEQUENCE 729 AA; 83351 MW; 6EBF07508CA9961F CRC64;

Query Match  
 Best Local Similarity 60.8%; Score 45; DB 2; Length 729;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKEAYKAAAP 14  
 ||:|:|  
 DB 290 KPEVDGYKGAAP 302

RESULT 13  
 SSB\_SHEON  
 ID SSB\_SHEON STANDARD; PRT; 238 AA.

AC Q8EA81;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Single-strand binding protein (SSB) (Helix-destabilizing protein).  
 GN Name=ssb; OrderedLocNames=SO4028;  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Shewanellaceae; Shewanella.  
 OX NCBI\_TaxID=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MR-1;  
 RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,  
 RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,  
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,  
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprial M.,  
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,  
 RA Venter J.C., Nealsen K.H., Fraser C.M.;  
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT Shewanella oneidensis.";  
 RL Nat. Biotechnol. 20:1118-1123(2002).  
 CC -!- FUNCTION: This protein is essential for replication of the  
 CC chromosome. It is also involved in DNA recombination and repair  
 CC (by similarity).  
 CC -!- SIMILARITY: Contains 1 SSB domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AE015834; AAN57002.1; -  
 DR HSSP; P02339; 1KAW.  
 DR TIGR; SO4028; -  
 DR InterPro; IPR008994; Nucleic acid\_OB.  
 DR InterPro; IPR010913; SS\_binding.  
 DR InterPro; IPR000424; SSB\_protein.  
 DR Pfam; PF00436; SSB; 1.  
 DR TIGRFAMs; TIGR00621; ssb; 1.  
 DR PROSITE; PS50935; SSB; 1.  
 KW Complete proteome; DNA repair; DNA replication; DNA-binding.  
 FT DOMAIN 6 110 SSB.  
 SQ SEQUENCE 238 AA; 25773 MW; 72638282E1455594 CRC64;

Query Match 59.5%; Score 44; DB 1; Length 238;  
 Best Local Similarity 64.3%; Pred. No. 40;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPA 15  
 DB 200 KPAPAYQAPAPAPA 213

## RESULT 14

Q62L76

ID Q62L76 PRELIMINARY; PRT; 342 AA.

AC Q62L76; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Phosphate ABC transporter, periplasmic phosphate-binding protein.

GN Name=pts; ORFNames=BMA0780;

OS Burkholderia mallei ATCC 23344.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI\_TaxID=243160;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATC 23344;

RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,

RA Feldblyum T., Ulrich R.L., Roming C.M., Brinkac L.M., Daugherty S.C.,

RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,

RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,

RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,

RA Selengut J., Shambhlin C., Sullivan S.A., White O., Yu Y., Zafar N.,

RA Zhou L., Fraser C.M.;

RT "Structural flexibility in the Burkholderia mallei genome.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

DR EMBL; CP000010; AAU49558.1; -

SQ SEQUENCE 342 AA; 36156 MW; E425E7A18B262B27 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 342;

Best Local Similarity 64.3%; Pred. No. 55;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPA 15

DB 238 EPKTETFKAAAAGA 251

## RESULT 15

Q63V82

ID Q63V82 PRELIMINARY; PRT; 342 AA.

AC Q63V82; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Phosphate transport system, substrate-binding exported periplasmic

DE protein.

GN Name=pts; Synonyms=phos; ORFNames=BPSL1359;

OS Burkholderia pseudomallei K96243.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI\_TaxID=272560;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K96243;

RX PubMed=15377794;

RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,

RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,

RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,

RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,

RA Chillingworth T., Cronin A., Croset B., Davis P., Deshazer D.,

RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,

RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,

RA Rabinowitch E., Rutherford K., Sanders M., Simmonds M.,

RA Songsiyilai S., Stevens K., Tumapa S., Vesaratchaveest M.,  
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,  
 RT "Genomic plasticity of the causative agent of melioidosis,  
 RT Burkholderia pseudomallei.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

DR EMBL; BX571965; CAH35357.1; -

SQ SEQUENCE 342 AA; 36156 MW; E425E7A18B262B27 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 342;  
 Best Local Similarity 64.3%; Pred. No. 55;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPA 15

DB 238 EPKTETFKAAAAGA 251

Search completed: February 26, 2005, 23:55:44  
 Job time : 66.2041 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 76.6837 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-86  
Perfect score: 76  
Sequence: 1 EAPKYEAAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	15	5	ABP52290 HLA-DR2 m
2	76	100.0	15	5	ABP52292 HLA-DR2 m
3	72	94.7	15	5	ABP52304 HLA-DR2 m
4	71	93.4	15	5	ABP52291 HLA-DR2 m
5	68	89.5	15	5	ABP52305 HLA-DR2 m
6	67	88.2	15	5	ABP52297 HLA-DR2 m
7	66	86.8	15	5	ABP52289 HLA-DR2 m
8	63	82.9	15	5	ABP52299 HLA-DR2 m
9	60	78.9	15	5	ABP52270 HLA-DR2 m
10	60	78.9	15	5	ABP52272 HLA-DR2 m
11	59	77.6	17	5	ABP52303 HLA-DR2 m
12	58	76.3	15	5	ABP52300 HLA-DR2 m
13	55	72.4	15	5	ABP52271 HLA-DR2 m
14	55	72.4	15	5	ABP52298 HLA-DR2 m
15	55	72.4	17	5	ABP52294 HLA-DR2 m
16	55	72.4	17	5	ABP52296 HLA-DR2 m
17	55	72.4	17	5	ABP52302 HLA-DR2 m
18	55	72.4	19	5	ABP52295 HLA-DR2 m
19	54	71.1	15	5	ABP52267 HLA-DR2 m
20	54	71.1	15	5	ABP52257 HLA-DR2 m
21	52	68.4	15	5	ABP52293 HLA-DR2 m
22	50	65.8	15	5	ABP52261 HLA-DR2 m
23	50	65.8	15	5	ABP52269 HLA-DR2 m
24	50	65.8	15	5	ABP52268 HLA-DR2 m
25	49	64.5	15	5	ABP52265 HLA-DR2 m

26	49	64.5	15	5	ABP52240	Abp52240 HLA-DR2 m
27	49	64.5	15	5	ABP52241	Abp52241 HLA-DR2 m
28	49	64.5	15	5	ABP52249	Abp52249 HLA-DR2 m
29	49	64.5	15	5	ABP52263	Abp52263 HLA-DR2 m
30	48	63.2	15	5	ABP52243	Abp52243 HLA-DR2 m
31	48	63.2	15	5	ABP52258	Abp52258 HLA-DR2 m
32	48	63.2	15	5	ABP52260	Abp52260 HLA-DR2 m
33	47	61.8	15	5	ABP52301	Abp52301 HLA-DR2 m
34	47	61.8	105	4	ABP52293	Abp52293 Drosophil
35	47	61.8	781	8	ADN60395	Adn60395 B. lichen
36	47	61.8	781	8	ADN60505	Adn60505 B. lichen
37	47	61.8	781	8	ADN60519	Adn60519 B. lichen
38	46	60.5	15	5	ABP52255	Abp52255 HLA-DR2 m
39	46	60.5	15	5	ABP52251	Abp52251 HLA-DR2 m
40	46	60.5	15	5	ABP52239	Abp52239 HLA-DR2 m
41	46	60.5	99	4	ABP52290	Abp52290 Drosophil
42	45.5	59.9	815	5	ADP93027	Adp93027 Thermus s
43	45.5	59.9	815	5	ADP93029	Adp93029 Thermus s
44	45.5	59.9	831	5	ADP93037	Adp93037 Thermus s
45	45.5	59.9	838	5	ADP92947	Adp92947 Construct

ALIGNMENTS

RESULT 1	ABP52290	standard; peptide; 15 AA.
ID	ABP52290	
XX	ABP52290;	
AC	16-OCT-2002	(first entry)
DT	HLA-DR2	molecule binding peptide SEQ ID NO:84.
DE	Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.	
XX	Homo sapiens.	
OS	Synthetic.	
PN	WO200259143-A2.	
XX	01-AUG-2002.	
PD	24-JAN-2002; 2002WO-US002071.	
PF	24-JAN-2001; 2001US-0263569P.	
PR	(HARD ) HARVARD COLLEGE.	
XX	Strominger JL, Fridkis-Hareli M;	
PI	WPI; 2002-608439/65.	
XX	New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.	
PT	Claim 28; Page 39; 54pp; English.	
PS	The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases	

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
SQ Sequence 15 AA;  
OY  
Query Match 100.0%; Score 76; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 EAPKYEAYKAAAPAA 15  
1 EAPKYEAYKAAAPAA 15  
RESULT 2  
ABP52292  
ID ABP52292 standard; peptide; 15 AA.  
XX  
AC ABP52292;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 15 AA;  
OY  
Query Match 100.0%; Score 76; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 EAPKYEAYKAAAPAA 15  
1 EAPKYEAYKAAAPAA 15  
RESULT 3  
ABP52304  
ID ABP52304 standard; peptide; 15 AA.  
XX  
AC ABP52304;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:98.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
OY  
Query Match 94.7%; Score 72; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3.8e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EAPKYEAYKAAAPAA 15

Db 1 EAPKFEAYKAAAPA 15  
| | | | | | | | | |  
| | | | | | | | | |  
RESULT 4  
ABP52291  
ID ABP52291 standard; peptide; 15 AA.  
XX  
AC ABP52291;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; page 39; 54pp; English.  
XX  
CC The present invention describes compositions (i) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (i) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 93.4%; Score 71; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 5.6e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EAPKFEAYKAAAPA 15  
| | | | | | | | | |  
| | | | | | | | | |  
Db 1 EAPKFEAYKAAAPA 15  
| | | | | | | | | |  
| | | | | | | | | |  
RESULT 5  
ABP52305  
ID ABP52305 standard; peptide; 15 AA.

XX  
AC ABP52305;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:99.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (i) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (i) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 89.5%; Score 68; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00018;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EAPKFEAYKAAAPA 15  
| | | | | | | | | |  
| | | | | | | | | |  
Db 1 EAPKFEAYKAAAPA 15  
| | | | | | | | | |  
| | | | | | | | | |  
RESULT 6  
ABP52297  
ID ABP52297 standard; peptide; 15 AA.  
XX  
AC ABP52297;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.  
XX

XX	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW	immune response; antiinflammatory; neuroprotective; proliferation;
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX	anti-tumour necrosis factor agent.
OS	Homo sapiens.
OS	Synthetic.
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
XX	24-JAN-2002; 2002WO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
XX	(HARD ) HARVARD COLLEGE.
XX	
PI	Strominger JL, Frickie-Hareli M;
PI	WPL; 2002-608439/65.
XX	
DR	
XX	New compositions comprising synthetic peptides in complex with a major
PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral
PT	encephalomyelitis.
XX	
PS	Claim 28; Page 39; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	demyelinating condition, and a side effect of administering an anti-
CC	tumour necrosis factor agents. The peptide further inhibits proliferation
CC	of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC	ABP52305 represent peptides used in the exemplification of the present
CC	invention
CC	
XX	
SQ	Sequence 15 AA;
	Query Match 88.2%; Score 67; DB 5; Length 15;
	Best Local Similarity 86.7%; Pred. No. 0.00026;
	Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 EAPKVEAYKKAAPA 15
DB	1 EKPKFEAYKKAAPA 15
RESULT 7	
ABP52289	
ID	ABP52289 standard; peptide; 15 AA.
XX	
AC	ABP52289;
XX	
DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:83.
XX	
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW	immune response; antiinflammatory; neuroprotective; proliferation;
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW	anti-tumour necrosis factor agent.
XX	

OS	Homo sapiens.
OS	Synthetic.
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
Pf	24-JAN-2002; 2002WO-US002071.
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD ) HARVARD COLLEGE.
XX	
PI	Strominger JL, Fridkis-Hareli M;
XX	
DR	WPI; 2002-608439/65.
XX	
PT	New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
PT	
PS	Claim 28; Page 39; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention
CC	
CC	
CC	
XX	
SEQ	Sequence 15 AA;
Query Match	86.8%; Score 66; DB 5; Length 15;
Best Local Similarity	86.7%; Pred. No. 0.00038;
Matches 13; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
Oy	1 EAPKYEAAYKAAAPA 15      :       1 EAPAYKAYKAAAPA 15
Db	
RESULT 8	
ABP52299	
ID	ABP52299 standard; peptide; 15 AA.
XX	
AC	ABP52299;
XX	
DT	16-OCT-2002 (first entry)
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:93.
XX	
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
KW	
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI, 2002-608439/65.  
DR  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 82.9%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0012;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 EAPKYEAAYKAAAPAA 15  
1 |||||  
Db 1 EAPKYEAAYKAAAPAA 15  
1 EAPKYEAAYKAAAPAA 15  
RESULT 9  
ABP52270  
ID ABP52270 standard; peptide; 15 AA.  
XX  
XX AC ABP52270;  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:64.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI

XX  
XX WPI, 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 78.9%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0039;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 EAPKYEAAYKAAAPAA 15  
1 |||||  
Db 1 EAPKYEAAYKAAAPAA 15  
1 EAPKYEAAYKAAAPAA 15  
RESULT 10  
ABP52272  
ID ABP52272 standard; peptide; 15 AA.  
XX  
XX AC ABP52272;  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:66.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI, 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
PI

XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX SQ Sequence 15 AA;  
XX  
XX Query Match 78.9%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0039;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAPKYEAYKAAAPPA 15  
DB 1 EAKKYEAYKAAAAA 15  
RESULT 11  
ABP52303  
ID ABP52303 standard; peptide; 17 AA.  
XX AC ABP52303;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX OS Homo sapiens.  
OS Synthetic.  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX SQ Sequence 17 AA;  
XX  
XX Query Match 77.6%; Score 59; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0066;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAPKYEAYKAAAPPA 15  
DB 3 EAKKYEAYKAAAAA 17  
RESULT 12  
ABP52300  
ID ABP52300 standard; peptide; 15 AA.  
XX AC ABP52300;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:94.  
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX OS Homo sapiens.  
OS Synthetic.  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 15 AA;

Query Match 76.3%; Score 58; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0084;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EAPKYEAYKAAAPAA 15  
| | | | | | | | | | | | | | |  
Db 1 EKPKKEAFKAAAPAA 15

## RESULT 13

ABP52271  
ID ABP52271 standard; peptide; 15 AA.

XX AC ABP52271;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.  
OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

SQ Sequence 15 AA;

Query Match 72.4%; Score 55; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.027;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAPKYEAYKAAAPAA 15  
| | | | | | | | | | | | | | |  
Db 1 EKAKEAYKAAAPAA 15

## RESULT 14

ABP52298  
ID ABP52298 standard; peptide; 15 AA.

XX AC ABP52298;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:92.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.  
OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

SQ Sequence 15 AA;

Query Match 72.4%; Score 55; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.027;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAPKYEAYKAAAPAA 15  
| | | | | | | | | | | | | | |  
Db 1 EKAKEAYKAAAPAA 15

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RESULT 15
ABP52294
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
XX
Query Match 72.4%; Score 55; DB 5; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAPKYEAYKAAAPA 15
| | | | | | | | | |
Db 3 EKAKYEAYKAAAAA 17
```

Search completed: February 26, 2005, 23:48:22  
Job time : 77.6837 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 20.051 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-86  
Perfect score: 76  
Sequence: 1 EAPKYEAAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued Patents AA:\*  
2: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	55.3	287	3	US-09-105-697-7
2	42	55.3	287	3	US-09-105-697-8
3	42	55.3	288	3	US-09-105-697-3
4	42	55.3	291	3	US-09-105-697-4
5	42	55.3	291	3	US-09-105-697-5
6	42	55.3	291	3	US-09-105-697-6
7	42	55.3	830	1	US-07-977-434-6
8	42	55.3	830	1	US-08-458-819-6
9	42	55.3	830	5	PCT-US91-07035-6
10	42	55.3	831	1	US-08-073-384C-5
11	42	55.3	831	1	US-08-254-359A-5
12	42	55.3	831	1	US-08-483-043-5
13	42	55.3	831	1	US-08-481-238-5
14	42	55.3	831	2	US-08-471-066B-5
15	42	55.3	831	2	US-08-484-956-5
16	42	55.3	831	2	US-08-484-956-5
17	42	55.3	831	2	US-08-599-491-5
18	42	55.3	831	2	US-08-756-386-5
19	42	55.3	831	2	US-08-823-516-5
20	42	55.3	831	3	US-08-682-853A-5
21	42	55.3	831	3	US-08-759-038-5
22	42	55.3	831	3	US-08-758-314-5
23	42	55.3	831	3	US-09-350-309-5
24	42	55.3	831	3	US-08-520-946-5
25	42	55.3	831	4	US-09-684-938-5
26	42	55.3	831	4	US-09-308-825A-5
27	42	55.3	831	4	US-09-758-282B-5

28	42	55.3	831	4	US-09-655-378A-5	Sequence 5, Appli
29	42	55.3	831	4	US-09-940-244-5	Sequence 5, Appli
30	42	55.3	831	4	US-09-333-145-5	Sequence 5, Appli
31	42	55.3	831	4	US-09-577-304A-5	Sequence 251, App
32	42	55.3	832	4	US-09-758-282B-251	Sequence 251, App
33	42	55.3	832	4	US-09-758-282B-268	Sequence 251, App
34	42	55.3	832	4	US-09-577-304A-251	Sequence 251, App
35	42	55.3	832	4	US-09-577-304A-268	Sequence 251, App
36	42	55.3	833	1	US-08-073-384C-8	Sequence 8, Appli
37	42	55.3	833	1	US-08-254-359A-8	Sequence 8, Appli
38	42	55.3	833	1	US-08-483-043-8	Sequence 8, Appli
39	42	55.3	833	1	US-08-481-238-8	Sequence 8, Appli
40	42	55.3	833	2	US-08-471-066B-8	Sequence 8, Appli
41	42	55.3	833	2	US-08-484-956-8	Sequence 8, Appli
42	42	55.3	833	2	US-08-757-653-8	Sequence 8, Appli
43	42	55.3	833	2	US-08-599-491-8	Sequence 8, Appli
44	42	55.3	833	2	US-08-756-386-8	Sequence 8, Appli
45	42	55.3	833	2	US-08-823-516-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-105-697-7  
; Sequence 7, Application US/09105697  
; Patent No. 6228628  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand Ph.D., David H.  
; APPLICANT: Reichert, Fred L.  
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Roche Molecular Systems  
; STREET: 1080 U.S. Highway 202  
; CITY: Branchburg  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08876  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,697  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry Ph.D., Douglas A.  
; REGISTRATION NUMBER: 35321  
; REFERENCE/DOCKET NUMBER: 1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510)814-2974  
; TELEFAX: (510)814-2977  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 287 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-105-697-7  
Query Match 55.3%; Score 42; DB 3; Length 287;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 YEAYKAAAP 14  
|||||  
Db 75 YEAYKAGRAP 84

## RESULT 2

US-09-105-697-8

Sequence 8, Application US/09105697

Patent No. 6228628

GENERAL INFORMATION:

APPLICANT: Gelfand Ph.D., David H.

APPLICANT: Reichert, Fred L.

TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Roche Molecular Systems

STREET: 1080 U.S. Highway 202

CITY: Branchburg

STATE: New Jersey

COUNTRY: United States

ZIP: 08876

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,697

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Petry Ph.D., Douglas A.

REGISTRATION NUMBER: 35321

REFERENCE/DOCKET NUMBER: 1043

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510)814-2974

TELEFAX: (510)814-2977

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 287 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-105-697-8

Query Match 55.3%; Score 42; DB 3; Length 287;

Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14

Db 75 YEAYKAGRAP 84

## RESULT 3

US-09-105-697-3

Sequence 3, Application US/09105697

Patent No. 6228628

GENERAL INFORMATION:

APPLICANT: Gelfand Ph.D., David H.

APPLICANT: Reichert, Fred L.

TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Roche Molecular Systems

STREET: 1080 U.S. Highway 202

CITY: Branchburg

STATE: New Jersey

COUNTRY: United States

ZIP: 08876

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,697

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Petry Ph.D., Douglas A.

REGISTRATION NUMBER: 35321

REFERENCE/DOCKET NUMBER: 1043

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510)814-2974

TELEFAX: (510)814-2977

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-105-697-3

Query Match 55.3%; Score 42; DB 3; Length 288;

Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14

Db 77 YEAYKAGRAP 86

## RESULT 4

US-09-105-697-4

Sequence 4, Application US/09105697

Patent No. 6228628

GENERAL INFORMATION:

APPLICANT: Gelfand Ph.D., David H.

APPLICANT: Reichert, Fred L.

TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Roche Molecular Systems

STREET: 1080 U.S. Highway 202

CITY: Branchburg

STATE: New Jersey

COUNTRY: United States

ZIP: 08876

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,697

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Petry Ph.D., Douglas A.

REGISTRATION NUMBER: 35321

REFERENCE/DOCKET NUMBER: 1043

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510)814-2974

TELEFAX: (510)814-2977

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 291 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-105-697-4

Query Match 55.3%; Score 42; DB 3; Length 291;

Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14

|||||  
Db 79 YEAYKAGRAP 88

## RESULT 5

US-09-105-697-5  
; Sequence 5, Application US/09105697  
; Patent No. 6228628  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand Ph.D., David H.  
; APPLICANT: Reichert, Fred L.  
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Roche Molecular Systems  
; STREET: 1080 U.S. Highway 202  
; CITY: Branchburg  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08876  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,697  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry Ph.D., Douglas A.  
; REGISTRATION NUMBER: 35321  
; REFERENCE/DOCKET NUMBER: 1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510)814-2974  
; TELEFAX: (510)814-2977  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 291 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-105-697-5

Query Match 55.3%; Score 42; DB 3; Length 291;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAP 14  
|||||  
Db 79 YEAYKAGRAP 88

## RESULT 6

US-09-105-697-6  
; Sequence 6, Application US/09105697  
; Patent No. 6228628  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand Ph.D., David H.  
; APPLICANT: Reichert, Fred L.  
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Roche Molecular Systems  
; STREET: 1080 U.S. Highway 202  
; CITY: Branchburg  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08876  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,697  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry Ph.D., Douglas A.  
; REGISTRATION NUMBER: 35321  
; REFERENCE/DOCKET NUMBER: 1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510)814-2974  
; TELEFAX: (510)814-2977  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 291 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-105-697-6

Query Match 55.3%; Score 42; DB 3; Length 291;  
Best Local Similarity 80.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAP 14  
|||||  
Db 79 YEAYKAGRAP 88

## RESULT 7

US-07-977-434-6  
; Sequence 6, Application US/07977434  
; Patent No. 546591  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand, David H.  
; APPLICANT: Abramson, Richard D.  
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; ZIP: 07110-1199  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: 7  
; SOFTWARE: WordPerfect 2.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,434  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,490  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,466  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,213  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 523,394  
; FILING DATE: 15-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 143,441  
; FILING DATE: 12-JAN-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 063,509

FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Cserr  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 830 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-977-434-6

Query Match 55.3%; Score 42; DB 1; Length 830;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14  
Db 75 YEAYKAGRAP 84

RESULT 8  
US-08-458-819-6  
Sequence 6, Application US/08458819  
Patent No. 5795762  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7  
SOFTWARE: WordPerfect 2.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,819  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/977,434  
FILING DATE: 23-FEB-1993

APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Cserr  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 5795762 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 830 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-819-6

Query Match 55.3%; Score 42; DB 1; Length 830;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14  
Db 75 YEAYKAGRAP 84

RESULT 9  
PCT-US91-07035-6  
Sequence 6, Application PC/TUS9107035  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cetus Corporation  
STREET: 1400 Fifty-third Street

CITY: Emeryville  
STATE: California  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07035  
FILING DATE: 19910930  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Sias Ph.D, Stacey R.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: Case No. 2580  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-420-3300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 830 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-07035-6

Query Match 55.3%; Score 42; DB 5; Length 830;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 YEAYKAAAP 14  
|||  
Db 75 YEAYKAGRAP 84

RESULT 10  
US-08-073-384C-5  
Sequence 5, Application US/08073384C  
Patent No. 5541311  
GENERAL INFORMATION:  
APPLICANT: Dahlberg, James E.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,384C  
FILING DATE: 04-JUN-1993  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/986,330  
FILING DATE: 07-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-00613  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/705-8410  
TELEFAX: 415/397-8338  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 831 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-073-384C-5

Query Match 55.3%; Score 42; DB 1; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 YEAYKAAAP 14  
|||  
Db 77 YEAYKAGRAP 86

RESULT 11  
US-08-254-359A-5  
Sequence 5, Application US/08254359A  
Patent No. 5614402  
GENERAL INFORMATION:  
APPLICANT: DAHLBERG, JAMES E.  
APPLICANT: LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/254,359A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,384  
FILING DATE: 06-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/986,330  
FILING DATE: 07-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01000  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 831 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-254-359A-5

Query Match 55.3%; Score 42; DB 1; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 YEAYKAAAP 14  
Db 77 YEAYKAGRAP 86

RESULT 12  
US-08-483-043-5  
Sequence 5, Application US/08483043  
Patent No. 5691142  
GENERAL INFORMATION:  
APPLICANT: Dahlberg, James E.  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA  
TITLE OF INVENTION: POLYMERASE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,043  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,384  
FILING DATE: 04-JUN-1993  
APPLICATION NUMBER: US 07/986,330  
FILING DATE: 07-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-00613  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/705-8410  
TELEFAX: 415/397-8338  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 831 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-043-5

Query Match 55.3%; Score 42; DB 1; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 YEAYKAAAP 14  
Db 77 YEAYKAGRAP 86

RESULT 13  
US-08-481-238-5  
Sequence 5, Application US/08481238  
Patent No. 5795763  
GENERAL INFORMATION:  
APPLICANT: DAHLBERG, JAMES E.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: BROW, MARY ANN D.  
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA  
TITLE OF INVENTION: POLYMERASE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,238  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 831 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-481-238-5

Query Match 55.3%; Score 42; DB 1; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 YEAYKAAAP 14

DB 77 YEAYKAGRAP 86

## RESULT 14

US-08-471-066B-5  
; Sequence 5, Application US/08471066B  
; Patent No. 5837450  
; GENERAL INFORMATION:  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Lyamichev, Victor I.  
; TITLE OF INVENTION: 5' Nucleases Derived From Thermostable  
; TITLE OF INVENTION: DNA Polymerase  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,066B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/254,359  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,384  
; FILING DATE: 04-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/986,330  
; FILING DATE: 07-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: FORS-01800  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 831 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-066B-5

Query Match 55.3%; Score 42; DB 2; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14  
DB 77 YEAYKAGRAP 86

RESULT 15  
US-08-484-956-5  
; Sequence 5, Application US/08484956  
; Patent No. 5843654  
; GENERAL INFORMATION:  
; APPLICANT: DAHLBERG, JAMES E.  
; APPLICANT: LYAMICHEV, VICTOR I.  
; APPLICANT: BROW, MARY ANN D.

; APPLICANT: OLDENBURG, MARY C.  
; APPLICANT: HEISLER, LAURA  
; TITLE OF INVENTION: DETECTION OF p53 MUTATIONS  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,956  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/402,601  
; FILING DATE: 09-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,164  
; FILING DATE: 09-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/254,359  
; FILING DATE: 06-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,384  
; FILING DATE: 04-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/986,330  
; FILING DATE: 07-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL J, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01801  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 831 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-484-956-5

Query Match 55.3%; Score 42; DB 2; Length 831;  
Best Local Similarity 80.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14  
DB 77 YEAYKAGRAP 86

Search completed: February 26, 2005, 23:59:28  
Job time : 21.051 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 53.5714 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-86  
Perfect score: 76  
Sequence: 1 EAPKYEA YKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	14	US-10-056-583-84 Sequence 84, Appl
2	76	100.0	15	14	US-10-056-583-86 Sequence 86, Appl
3	72	94.7	15	14	US-10-056-583-98 Sequence 98, Appl
4	71	93.4	15	14	US-10-056-583-85 Sequence 85, Appl
5	68	89.5	15	14	US-10-056-583-99 Sequence 99, Appl
6	67	88.2	15	14	US-10-056-583-91 Sequence 91, Appl
7	66	86.8	15	14	US-10-056-583-83 Sequence 83, Appl
8	63	82.9	15	14	US-10-056-583-93 Sequence 93, Appl
9	60	78.9	15	14	US-10-056-583-64 Sequence 64, Appl
10	60	78.9	15	14	US-10-056-583-66 Sequence 66, Appl
11	59	77.6	17	14	US-10-056-583-97 Sequence 97, Appl
12	58	76.3	15	14	US-10-056-583-94 Sequence 94, Appl
13	55	72.4	15	14	US-10-056-583-65 Sequence 65, Appl

	14	55	72.4	17	14	US-10-056-583-88	Sequence 88, Appl
	15	55	72.4	17	14	US-10-056-583-90	Sequence 90, Appl
	16	55	72.4	17	14	US-10-056-583-96	Sequence 96, Appl
	17	55	72.4	19	14	US-10-056-583-89	Sequence 89, Appl
	18	54	71.1	15	14	US-10-056-583-51	Sequence 51, Appl
	19	54	71.1	15	14	US-10-056-583-61	Sequence 61, Appl
	20	52	68.4	15	14	US-10-056-583-87	Sequence 87, Appl
	21	50	65.8	15	14	US-10-056-583-55	Sequence 55, Appl
	22	50	65.8	15	14	US-10-056-583-62	Sequence 62, Appl
	23	50	65.8	15	14	US-10-056-583-63	Sequence 63, Appl
	24	49	64.5	15	14	US-10-056-583-34	Sequence 34, Appl
	25	49	64.5	15	14	US-10-056-583-35	Sequence 35, Appl
	26	49	64.5	15	14	US-10-056-583-43	Sequence 43, Appl
	27	49	64.5	15	14	US-10-056-583-57	Sequence 57, Appl
	28	49	64.5	15	14	US-10-056-583-59	Sequence 59, Appl
	29	48	63.2	15	14	US-10-056-583-37	Sequence 37, Appl
	30	48	63.2	15	14	US-10-056-583-52	Sequence 52, Appl
	31	48	63.2	15	14	US-10-056-583-95	Sequence 95, Appl
	32	47	61.8	15	14	US-10-056-583-33	Sequence 33, Appl
	33	46	60.5	15	14	US-10-056-583-45	Sequence 45, Appl
	34	46	60.5	15	14	US-10-056-583-45	Sequence 45, Appl
	35	46	60.5	15	14	US-10-056-583-49	Sequence 49, Appl
	36	46	60.5	15	14	US-10-056-583-92	Sequence 92, Appl
	37	45.5	59.9	815	10	US-09-864-636A-580	Sequence 580, App
	38	45.5	59.9	815	10	US-09-864-636A-582	Sequence 582, App
	39	45.5	59.9	815	11	US-09-864-426A-580	Sequence 580, App
	40	45.5	59.9	815	11	US-09-864-426A-582	Sequence 582, App
	41	45.5	59.9	815	14	US-10-084-839-580	Sequence 580, App
	42	45.5	59.9	815	14	US-10-084-839-582	Sequence 582, App
	43	45.5	59.9	815	14	US-10-084-839-2827	Sequence 2827, Ap
	44	45.5	59.9	815	14	US-10-084-839-2829	Sequence 2829, Ap
	45	45.5	59.9	831	10	US-09-864-636A-590	Sequence 590, App

## ALIGNMENTS

RESULT 1  
US-10-056-583-84  
; Sequence 84, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-84

Query Match 100.0%; Score 76; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAPKYEA YKAAAPA 15  
Db 1 EAPKYEA YKAAAPA 15

RESULT 2  
US-10-056-583-86

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; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86
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Query Match          100.0%; Score 76; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 EAPKYEAYKAAAPAA 15
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Db      1 EAPKYEAYKAAAPAA 15
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## RESULT 3

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US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98
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Query Match          94.7%; Score 72; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      1 EAPKYEAYKAAAPAA 15
        |||||
Db      1 EAPKYEAYKAAAPAA 15
```

## RESULT 4

```
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
```

```
Query Match          93.4%; Score 71; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EAPKYEAYKAAAPAA 15
        |||||
Db      1 EAPKYEAYKAAAPAA 15
```

## RESULT 5

```
US-10-056-583-99
; Sequence 99, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
```

```
Query Match          89.5%; Score 68; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EAPKYEAYKAAAPAA 15
        |||||
Db      1 EAPKYEAYKAAAPAA 15
```

## RESULT 6

```
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
```

```
Query Match      88.2%; Score 67; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00026;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAPKYEAYKAAAPAA 15
        |||:|||||
Db       1 EKPKFEAYKAAAPAA 15
```

```
RESULT 7
US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-83
```

```
Query Match      86.8%; Score 66; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00039;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAPKYEAYKAAAPAA 15
        |||:|||||
Db       1 EAPAYKAYKAAAPAA 15
```

```
RESULT 8
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93
```

```
Query Match      82.9%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 EAPKYEAYKAAAPAA 15
        |||:|||||
Db       1 EKPKVEAYKAAAPAA 15
```

```
RESULT 9
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match      78.9%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 EAPKYEAYKAAAPAA 15
        |||:|||||
Db       1 EAAKYEAYKAAAAAA 15
```

```
RESULT 10
US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 78.9%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0037;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPAA 15  
|||:|||||  
Db 1 EAKKYEAAYKAAAPAA 15

RESULT 11  
US-10-056-583-97

Sequence 97, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-97

Query Match 77.6%; Score 59; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0062;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPAA 15  
|||:|||||  
Db 3 EAKKYEAAYKAAAPAA 17

RESULT 12  
US-10-056-583-94

Sequence 94, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 94  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-94

Query Match 76.3%; Score 58; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.008;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPAA 15  
|||:|||||  
Db 1 EKPKEAFKAAAPAA 15

RESULT 13  
US-10-056-583-65

Sequence 65, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 65  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-65

Query Match 72.4%; Score 55; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.028;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPAA 15  
|||:|||||  
Db 1 EAKKYEAAYKAAAPAA 15

RESULT 14  
US-10-056-583-88

Sequence 88, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 88  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-88

Query Match 72.4%; Score 55; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.028;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPAA 15  
|||:|||||  
Db 3 EAKKYEAAYKAAAPAA 17

## RESULT 15

US-10-056-583-90

; Sequence 90, Application US/10056583

; Publication No. US20030064915A1

## ; GENERAL INFORMATION:

; APPLICANT: Presidents and Fellows of Harvard College

; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/10/056,583

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 90

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-90

## Query Match

72.4%; Score 55; DB 14; Length 17;

Best Local Similarity 80.0%; Pred. No. 0.028;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPAA 15

Db 1 EKAKYEAYKAAAPAA 15

Search completed: February 27, 2005, 00:05:22  
Job time : 53.5714 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 13.3163 Seconds  
(without alignments)  
108.382 Million cell updates/sec

Title: US-10-056-583A-86  
Perfect score: 76  
Sequence: 1 EAPKYEAAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	57.9	193	1	MOMS4E myosin alkali ligh
2	43	56.6	168	2	A45943 vitelline membrane
3	42	55.3	185	1	MOC4E myosin alkali ligh
4	42	55.3	188	2	IS0145 homeotic protein H
5	42	55.3	195	2	S28845 myosin regulatory
6	42	55.3	289	2	A43562 homeotic protein H
7	42	55.3	306	2	G96014 hypothetical prote
8	42	55.3	428	2	E87463 hypothetical prote
9	42	55.3	831	2	S26675 DNA-directed DNA p
10	41	53.9	188	2	A23253 myosin AI catalyti
11	41	53.9	193	1	MORT4E myosin alkali ligh
12	41	53.9	261	2	TS1222 hypothetical prote
13	41	53.9	336	2	B81081 tryptophanyl-trNA
14	41	53.9	336	2	E81863 tryptophan-trNA li
15	40.5	53.3	447	2	AB3359 dihydroliipoamide S
16	40	52.6	183	1	AZNMG azurin precursor -
17	40	52.6	183	1	AZNMH azurin precursor
18	40	52.6	183	2	A81072 azurin precursor N
19	40	52.6	183	2	E81797 azurin precursor N
20	40	52.6	316	2	T31880 hypothetical prote
21	40	52.6	389	2	G87332 hypothetical prote
22	40	52.6	518	2	D69813 ABC transporter (A
23	39.5	52.0	115	2	G72568 hypothetical prote
24	39.5	52.0	392	2	C72427 pyruvate synthase
25	39	51.3	197	1	MOH4E myosin alkali ligh
26	39	51.3	361	2	T12470 hypothetical prote
27	39	51.3	405	1	XUECD dihydroliipoamide S
28	39	51.3	405	2	G85573 dihydroliipoamide S
29	39	51.3	405	2	H90722 dihydroliipoamide S

30	39	51.3	546	2	T06415 calnexin - soybean
31	39	51.3	579	2	B84956 cell division prot
32	39	51.3	581	2	AD0727 penicillin-binding
33	39	51.3	1004	2	B25039 outer cell wall pr
34	39	51.3	1857	1	S01787 fatty-acid synthas
35	38	50.0	114	2	G81353 hypothetical prote
36	38	50.0	192	1	MOC4LA myosin alkali ligh
37	38	50.0	239	2	H87057 conserved hypothet
38	38	50.0	404	2	AF2225 hypothetical prote
39	38	50.0	432	2	AF2801 hypothetical prote
40	38	50.0	438	2	H97580 hypothetical prote
41	38	50.0	438	2	G87675 arylesterase-relat
42	38	50.0	442	2	D36718 dihydroliipoamide S
43	38	50.0	461	2	A13358 pyruvate dehydroge
44	38	50.0	465	2	A47023 S-layer protein -
45	38	50.0	497	2	JE0275 voltage-gated pota

## ALIGNMENTS

RESULT 1  
MOMS4E  
myosin alkali light chain 4, embryonic and atrial - mouse  
N/Alternate names: MLC1A; MLC1emb; myosin LI catalytic light chain, atrial  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1990 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C/Accession: A31114; S01944  
R/Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Saasoon, D.; Weydert, A.; Buckingh  
J. Biol. Chem. 263, 12669-12676, 1988  
A/Title: Structure and sequence of the myosin alkali light chain gene expressed in adul  
A/Reference number: A31114; MUID:88315068; PMID:2842339  
A/Accession: A31114  
A/Molecule type: DNA  
A/Residues: 1-193 <BAR>  
A/Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:G199731; PIDN:  
R/Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.  
Nucleic Acids Res. 16, 10037-10052, 1988  
A/Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striat  
A/Reference number: S01944; MUID:89057447; PMID:3194193  
A/Accession: S01944  
A/Molecule type: DNA  
A/Residues: 1-41 <COH>  
A/Cross-references: EMBL:X12971; NID:G53138; PIDN:CAA31414.1; PID:G53139  
C/Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fe  
C/Genetics:  
A/Intons: 41/3; 51/1; 101/1; 159/1; 185/1  
C/Superfamily: calmodulin; calmodulin repeat homology  
C/Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contra  
F/47-81/Domain: calmodulin repeat homology <BF1>  
F/126-158/Domain: calmodulin repeat homology <EF3>  
F/161-193/Domain: calmodulin repeat homology <BF4>

Query Match 57.9%; Score 44; DB 1; Length 193;  
Best Local Similarity 76.9%; Pred. No. 5;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PRYEAYKAAAPA 15  
Db 8 PKKEAAPPAAAPA 20

RESULT 2  
A45943  
vitelline membrane protein 26A-4 precursor - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: A45943  
R/Popodi, E.; Minoo, P.; Burke, T.; Waring, G.L.  
Dev. Biol. 127, 248-256, 1988  
A/Title: Organization and expression of a second chromosome follicle cell gene cluster  
A/Reference number: A45943; MUID:88242923; PMID:3132408  
A/Accession: A45943

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-168 <POP>  
A;Cross-references: UNIPROT:P13238; GB:M20936; NID:g158728; PID:g158729  
C;Genetics:  
A;Gene: FlyBase:Vm26Ab  
A;Cross-references: FlyBase:FBgn0003980

Query Match 56.6%; Score 43; DB 2; Length 168;  
Best Local Similarity 64.3%; Pred. No. 6; 4;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAP 15  
Db 66 APAQAQYSAAPAPA 79

## RESULT 3

## MOCH4E

myosin alkali light chain 4, embryonic - chicken  
N;Alternate names: myosin L23 catalytic light chain  
C;Species: Gallus gallus (chicken)  
C;Date: 01-Dec-1989 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C;Accession: S02065; A29473

R;Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nomomura, Y.; Fujii-Kuriyama, Y.

J. Mol. Biol. 204, 497-505, 1988

A;Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic g

A;Reference number: S02065; MUID:89141751; PMID:3225843

A;Accession: S02065

A;Molecule type: DNA

A;Residues: 1-185 <NAB>  
A;Cross-references: UNIPROT:P09540; EMBL:X14428

A;Note: the authors translated the codon CCG for residue 71 as Ala

R;Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.

J. Biol. Chem. 262, 14408-14414, 1987

A;Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac

A;Reference number: A29473; MUID:88032983; PMID:3667580

A;Accession: A29473

A;Molecule type: mRNA

A;Residues: 1-93; 'L', 95-165, 'L', 167-185 <KAW>  
A;Cross-references: GB:J02823; NID:g212339; PIDN:AAA48957.1; PID:g212340

A;Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1

C;Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac

C;Genetics:

A;Introns: 33/3; 43/1; 93/1; 151/1; 177/1

C;Complex: The myosin molecule contains two heavy chains, two alkali light chains, and

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: brain; calcium binding; duplication; EF hand; muscle contraction

F;39-73/Domain: calmodulin repeat homology <EF1>  
F;118-150/Domain: calmodulin repeat homology <EF3>  
F;153-185/Domain: calmodulin repeat homology <EF4>

Query Match 55.3%; Score 42; DB 1; Length 185;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAP 14  
Db 8 PKKDAKAAAP 19

## RESULT 4

## I50145

homeotic protein Hox M - chicken  
N;Alternate names: CHOX M

C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
C;Accession: I50145; S14512

R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.

Leukemia 5, 357-360, 1991

A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viru

A;Reference number: I50145; MUID:91238215; PMID:1674560

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-188 <CRO>

A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g6270

C;Genetics:

A;Gene: CHOX M

C;Superfamily: homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;96-152/Domain: homeobox homology <HOX>

Query Match 55.3%; Score 42; DB 2; Length 188;  
Best Local Similarity 69.2%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAP 15  
Db 8 PLYSKYKAAAP 20

RESULT 5

S28845

myosin regulatory light chain LC25, muscle - earthworm (Lumbricus terrestris)

C;Species: Lumbricus terrestris (common earthworm)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S28845

R;Serre, M.; Meyer, H.E.; Craig, A.G.; Carlhoff, D.; d'Haese, J.

Eur. J. Biochem. 211, 341-346, 1993

A;Title: Complete amino acid sequence of the regulatory light chain of obliquely striat

A;Reference number: S28845; MUID:93145966; PMID:842543

A;Accession: S28845

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-195 <SER>

A;Cross-references: UNIPROT:P80164

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: EF hand

F;55-87/Domain: calmodulin repeat homology <EF1>

Query Match 55.3%; Score 42; DB 2; Length 195;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAP 15  
Db 16 DAPAEAPAAAP 30

## RESULT 6

## A43562

homeotic protein Hox D8 - mouse  
N;Alternate names: homeotic protein Hox 4.3

C;Species: Mus musculus (house mouse)  
C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: A43562

R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zapavigna, V.; Falkenstein, H.; Dubou

Development 110, 733-745, 1990

A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob

A;Reference number: A43562; MUID:91209232; PMID:1982431

A;Accession: A43562

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-289 <IZP>

A;Cross-references: UNIPROT:P23463

C;Superfamily: homeotic protein Hox A7; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;196-252/Domain: homeobox homology <HOX>

Db 8 PLYSKYKAAAAA 20

RESULT 7

G96014  
hypothetical protein (imported) - Sinorhizobium meliloti (strain 1021) megaplasmid pSymb  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G96014  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: G96014  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-306 <KUR>  
A:Cross-references: UNIPROT:Q92TW2; GB:AL591985; PIDN:CAC49783.1; PID:g15141270; GSPDB:C  
A:Experimental source: strain 1021, megaplasmid pSymb  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Smb20676  
A:Genome: plasmid

Query Match 55.3%; Score 42; DB 2; Length 306;  
Best Local Similarity 61.5%; Pred. No. 17;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAPA 15  
|:|:|:|:|:|:|  
Db 67 PQEAFESAAAPA 79

RESULT 8

E87463  
hypothetical protein CC1729 (imported) - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: E87463  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: E87463  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-428 <STO>  
A:Cross-references: UNIPROT:Q9A7J4; GB:AE005673; NID:g13423147; PIDN:AAK23705.1; GSPDB:C  
C:Genetics:  
A:Gene: CC1729  
C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 55.3%; Score 42; DB 2; Length 428;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAPA 13  
|:|:|:|:|:|:|  
Db 87 APKVEAPKAAAPA 98

RESULT 9

S26675

DNA-directed DNA polymerase (EC 2.7.7.7) I - Thermus aquaticus  
C:Species: Thermus aquaticus  
C:Date: 03-May-1994 #sequence\_revision 20-Feb-1995 #text\_change 18-Jun-1999  
C:Accession: S26675; S24929  
R:Akhmetzjanov, A.A.; Vakhitov, V.A.  
Nucleic Acids Res. 20, 5839, 1992  
A:Title: Molecular cloning and nucleotide sequence of the DNA polymerase gene from Ther.  
A:Reference number: S26675; MUID:93087201; PMID:1454544  
A:Accession: S26675  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-831 <AKH>  
A:Cross-references: EMBL:X66105; NID:g48165; PIDN:CAA46900.1; PID:g48166  
A:Note: the source is designated as Thermus flavus  
C:Genetics:  
A:Gene: polI  
C:Superfamily: DNA-directed DNA polymerase I  
C:Keywords: DNA binding; nucleotidyltransferase

Query Match 55.3%; Score 42; DB 2; Length 831;  
Best Local Similarity 80.0%; Pred. No. 45;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAP 14  
|:|:|:|:|:|:|  
Db 77 YEAYKAGRAP 86

RESULT 10

A23253  
myosin A1 catalytic light chain, skeletal muscle - mouse  
N:Alternate names: myosin alkali light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Jun-1987 #sequence\_revision 24-Jun-1987 #text\_change 13-Aug-1999  
C:Accession: A23253; S02259  
R:Robert, B.; Daubas, P.; Akimenko, M.A.; Cohen, A.; Garner, I.; Guenet, J.L.; Buckingh  
Cell 39, 129-140, 1984  
A:Title: A single locus in the mouse encodes both myosin light chains 1 and 3, a second  
A:Reference number: A90854; MUID:85024885; PMID:6091905  
A:Accession: A23253  
A:Molecule type: DNA  
A:Residues: 1-188 <ROB>  
A:Note: the authors translated the codon ATT for residue 173 as Asn  
R:Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.  
Nucleic Acids Res. 16, 10037-10052, 1988  
A:Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striat  
A:Reference number: S01944; MUID:89057447; PMID:3194193  
A:Accession: S02259  
A:Molecule type: DNA  
A:Residues: 1-38 <COH>  
A:Cross-references: EMBL:X12973; NID:g53140; PIDN:CAA31416.1; PID:g53141  
C:Genetics:  
A:Introns: 38/3; 48/1; 96/1; 154/1; 180/1  
C:Superfamily: calmodulin; calmodulin repeat homology  
C:Keywords: alternative splicing; calcium binding; EF hand; muscle; skeletal muscle  
F:44-76/Domain: calmodulin repeat homology <EF1>  
F:121-153/Domain: calmodulin repeat homology <EF2>

Query Match 53.9%; Score 41; DB 2; Length 188;  
Best Local Similarity 64.3%; Pred. No. 15;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 APKYEAYKAAAPA 15  
|:|:|:|:|:|:|  
Db 2 APKVDVKKPAAAPA 15

RESULT 11

MORT4E  
myosin alkali light chain 4, embryonic and atrial - rat  
N:Alternate names: MLC1A; MLC1emb; myosin I1 catalytic light chain, atrial  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Jan-1993 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004

C;Accession: S09236  
R;Reviewer, A.S.; McNally, E.M.; Leitwand, L.A.  
Nucleic Acids Res. 18, 1581-1586, 1990  
A;Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expression  
A;Reference number: S09236; MUID:90221887; PMID:2326197  
A;Accession: S09236  
A;Molecule type: mRNA  
A;Residues: 1-193 <ROV>  
A;Cross-references: UNIPROT:P17209; EMBL:X51531; NID:g57512; PIDN:CAA35911.1; PID:g57513  
C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fetal  
C;Superfamily: calmodulin, calmodulin repeat homology  
C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract  
F;47-81/Domain: calmodulin repeat homology <EF1>  
F;126-158/Domain: calmodulin repeat homology <EF3>  
F;161-193/Domain: calmodulin repeat homology <EF4>

Query Match 53.9%; Score 41; DB 1; Length 193;  
Best Local Similarity 69.2%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PKYEAYKAAAPPA 15  
||| |  
Db 8 PKKETAKVAAAPPA 20

RESULT 12  
T51222  
hypothetical protein B24M22.180 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 09-Jul-2004  
C;Accession: T51222  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A;Reference number: Z25286  
A;Accession: T51222  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-261 <SCH>  
A;Cross-references: UNIPROT:Q9P390; EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.180  
A;Experimental source: strain OR74A  
C;Genetics:  
A;Gene: NCSP:B24M22.180  
A;Map position: 6  
A;Introns: 250/1

Query Match 53.9%; Score 41; DB 2; Length 261;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 APKYEAAYKAAAPPA 15  
||| |  
Db 116 APKQEQSKAAAPPA 129

RESULT 13  
B81081  
tryptophanyl-tRNA synthetase NM81471 [imported] - Neisseria meningitidis (strain MC58 se  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: B81081  
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755; PMID:10710307  
A;Accession: B81081  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-336 <TET>  
A;Cross-references: UNIPROT:Q9JYQ9; GB:AE002496; GB:AE002098; NID:g7226701; PIDN:AAF4182  
A;Experimental source: serogroup B, strain MC58

C;Genetics:  
A;Gene: NM81471  
C;Superfamily: tryptophan-tRNA ligase

Query Match 53.9%; Score 41; DB 2; Length 336;  
Best Local Similarity 46.7%; Pred. No. 27;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPPA 15  
|:|:|:|:|:|:|:  
Db 243 ESPLFEIYKAFSTPS 257

RESULT 14  
E81863  
tryptophan-tRNA ligase (EC 6.1.1.2) NMA1682 [imported] - Neisseria meningitidis (strain  
C;Species: Neisseria meningitidis  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: E81863  
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A;Reference number: A81775; MUID:20222556; PMID:10761919  
A;Accession: E81863  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-336 <PAR>  
A;Cross-references: UNIPROT:Q9JYQ0; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8491  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: trps; NMA1682  
C;Superfamily: tryptophan-tRNA ligase  
C;Keywords: ligase

Query Match 53.9%; Score 41; DB 2; Length 336;  
Best Local Similarity 46.7%; Pred. No. 27;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAAYKAAAPPA 15  
|:|:|:|:|:|:|:  
Db 243 ESPLFEIYKAFSTPS 257

RESULT 15  
AB3359  
dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) [imported] - Brucella melitensis (str  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AB3359  
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,  
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes-  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AB3359  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-447 <KUR>  
A;Cross-references: UNIPROT:Q8YHES; GB:AE008917; PIDN:AAL52037.1; PID:g17982803; GSPDB:(  
A;Experimental source: strain 16M.  
C;Genetics:  
A;Gene: BMEI0856  
A;Map position: 1  
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
C;Keywords: acyltransferase; coenzyme A

Query Match 53.3%; Score 40.5; DB 2; Length 447;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 12; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

QY 1 EAPK-----YEAYKAAAPPA 15  
||| |

Db 98 EAPKDEPKPAEAKKEAAPA 117

Search completed: February 26, 2005, 23:57:14  
Job time : 15.3163 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 65.2041 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-86  
Perfect score: 76  
Sequence: 1 EAPKYEAAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	61.8	105	2	Q9VFV5	Q9VFV5 drosophila
2	47	61.8	294	2	Q93HV7	Q93HV7 arthrobacte
3	47	61.8	781	2	Q65JG3	Q65JG3 bacillus 11
4	46	60.5	99	2	Q9VAV6	Q9VAV6 drosophila
5	45	59.2	299	2	Q6Y8U4	Q6Y8U4 oryza sativ
6	45	59.2	408	2	Q7S7R7	Q7S7R7 neurospora
7	44	57.9	192	1	MLEF_MOUSE	P09541 mus musculu
8	44	57.9	316	2	Q6C9V2	Q6C9V2 yarrowia li
9	44	57.9	424	2	Q73BN9	Q73BN9 bacillus ce
10	44	57.9	439	2	Q869Y7	Q869Y7 dictyosteli
11	44	57.9	591	2	Q7WJF6	Q7WJF6 bordetella
12	44	57.9	802	2	Q8H1Y7	Q8H1Y7 hordeum vul
13	44	57.9	802	2	Q8H1Y8	Q8H1Y8 hordeum vul
14	43.5	57.2	277	1	RS3_STRCO	Q910d4 streptomyc
15	43	56.6	163	2	Q6JRS4	Q6JRS4 equus cabal
16	43	56.6	168	1	VTU2_DROME	P13238 drosophila
17	43	56.6	380	2	Q7PEG4	Q7PEG4 anopheles g
18	43	56.6	608	2	Q87T98	Q87T98 vibrio para
19	43	56.6	612	2	Q9Z6I4	Q9Z6I4 streptomyc
20	42	55.3	98	2	Q9LRI4	Q9LRI4 pisum sativ
21	42	55.3	185	1	MLEX_CHICK	P09540 gallus gall
22	42	55.3	188	1	HXB8_CHICK	P23459 gallus gall
23	42	55.3	195	1	MLR_LUMTE	P80164 lumbricus t
24	42	55.3	289	1	HXB8_MOUSE	P23463 mus musculu
25	42	55.3	289	2	Q8IXZ1	Q8IXZ1 homo sapien
26	42	55.3	290	1	HXB8_HUMAN	P13378 homo sapien
27	42	55.3	306	2	Q92TW2	Q92TW2 rhizobium m
28	42	55.3	356	2	Q6K4G2	Q6K4G2 oryza sativ
29	42	55.3	428	2	Q9A7J4	Q9A7J4 caulobacter
30	42	55.3	458	2	Q7SDS7	Q7SDS7 neurospora
31	42	55.3	548	2	Q87VD3	Q87VD3 pseudomonas

32	42	55.3	555	2	Q7NVT5	Q7NVT5 chromobacte
33	42	55.3	831	1	DP0F_THETH	P30313 thermus the
34	42	55.3	833	1	DP0I_THEFI	O52225 thermus fil
35	42	55.3	833	2	Q6X9R2	Q6X9R2 thermus fil
36	42	55.3	834	1	DP0I_THECA	P80194 thermus cal
37	42	55.3	834	1	DP0T_THETH	P52028 thermus the
38	42	55.3	834	2	Q72J58	Q72J58 thermus the
39	42	55.3	947	2	Q87YI0	Q87YI0 pseudomonas
40	41.5	54.6	214	2	Q88LD7	Q88LD7 pseudomonas
41	41.5	54.6	299	1	RL22_DROME	P50887 drosophila
42	41.5	54.6	312	2	Q9UAN1	Q9UAN1 drosophila
43	41	53.9	121	2	Q8LH24	Q8LH24 oryza sativ
44	41	53.9	121	2	Q8LI74	Q8LI74 oryza sativ
45	41	53.9	187	1	MLEI_MOUSE	P05977 mus musculu

ALIGNMENTS

RESULT 1						
ID	Q9VFV5	PRELIMINARY;	PRT;	105	AA.	
AC	Q9VFV5;					
DT	01-MAY-2000	(TREMBlrel. 13, Created)				
DT	01-MAY-2000	(TREMBlrel. 13, Last sequence update)				
DT	01-OCT-2002	(TREMBlrel. 22, Last annotation update)				
DE	CG14377-PA.					
GN	ORFNames=CG14377;					
OS	Drosophila melanogaster (Fruit fly).					
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
OC	Ephydroidea; Drosophilidae; Drosophila.					
OX	NCBI_TaxID=7227;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;					
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,					
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,					
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,					
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,					
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,					
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,					
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,					
RA	Ballew R.W., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,					
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,					
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,					
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,					
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,					
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,					
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,					
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,					
RA	Fosler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,					
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,					
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,					
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,					
RA	Jalali M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,					
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,					
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,					
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,					
RA	Merkulov G., Mileshina N.V., Mobarry C., Morris J., Moshrefi A.,					
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,					
RA	Nelson D.R., Nelson K.A., Nixon K., Nusker D.R., Pacle J.M.,					
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,					
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,					
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,					
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,					
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,					
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,					
RA	Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,					
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,					
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,					
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,					
RT	"The genome sequence of Drosophila melanogaster."					

RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnikier S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirska R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnikier S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Betman B.P.,  
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003700; AAF54944.1; -.  
DR FlyBase; FBgn0038148; CG14377.  
SQ SEQUENCE 105 AA; 10570 MW; BCE05E9DDBE35C5C CRC64;  
Query Match 61.8%; Score 47; DB 2; Length 105;  
Best Local Similarity 64.3%; Pred. No. 5.4;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2 APKYEAYKAAAPA 15  
Db 47 APSYSTYAAAVPA 60  
RESULT 2  
Q93HV7 PRELIMINARY; PRT; 294 AA.  
AC Q93HV7;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Probable dihydrodipicolinate acyltransferase (Fragment).  
OS Archaeobacter globiformis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococccineae; Micrococccaceae; Archaeobacter.  
OX NCBI\_TaxID=1665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hata H., Oshima Y., Ono K., Mori T., Kochi H.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 2 lipoyl-binding domains.

DR EMBL; AB056512; BAB64317.1; -.  
DR HSSP; P11961; 1LAB.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR004167; E3 binding.  
DR InterPro; IPR011053; Hybrid motif.  
DR InterPro; IPR003016; Lipoyl\_BS.  
DR Pfam; PF00364; Biotin\_lipoyl; 2.  
DR PROSITE; PS00189; LIPOYL; 2.  
KW Acyltransferase; Lipoyl; Transferase.  
FT NON TER 294  
SQ SEQUENCE 294 AA; 29117 MW; 82C80DE67E48B2B5 CRC64;  
Query Match 61.8%; Score 47; DB 2; Length 294;  
Best Local Similarity 73.3%; Pred. No. 15;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EAPKYEAYKAAAPA 15  
Db 225 EAPKQEAAPAPAAAPA 239  
RESULT 3  
Q65JG3 PRELIMINARY; PRT; 781 AA.  
AC Q65JG3;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE SpoIIIE (DNA translocase).  
GN Name=spoIIIE; ORFNames=BL01204, BL01906;  
OS Bacillus licheniformis DSM 13.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=279010;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 13;  
RX PubMed=15383718;  
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,  
RA Ehrenreich A., Gottschalk G.;  
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an  
RT Organism with Great Industrial Potential.";  
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14580;  
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,  
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,  
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,  
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,  
RA Berka R.M.;  
RT "Complete genome sequence of the industrial bacterium Bacillus  
RT licheniformis and comparisons with closely related Bacillus species.";  
RL Genome Biol. 5:R77-R77(2004).  
DR EMBL; AE017333; AAU40801.1; -.  
DR EMBL; CP000002; AAU23441.1; -.  
SQ SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;  
Query Match 61.8%; Score 47; DB 2; Length 781;  
Best Local Similarity 60.0%; Pred. No. 37;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EAPKYEAYKAAAPA 15  
Db 264 EKPEVQAYEAPAPAA 278  
RESULT 4

Q9VFV6 ;  
ID Q9VFV6 PRELIMINARY; PRT; 99 AA.  
AC Q9VFV6;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE CG14374-PA.  
GN ORFNames=CG14374;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadiou E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,  
RA Foster C., Gabrieli A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
RA Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Belencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003700; AAF54943.1; -.  
DR IntAct; Q9VFV6; -.  
DR FlyBase; FBgn0040553; CG14374.  
SQ SEQUENCE 99 AA; 9867 MW; 71E100667F009D76 CRC64;  
Query Match 60.5%; Score 46; DB 2; Length 99;  
Best Local Similarity 64.3%; Pred. No. 7.5;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2 APKYEAYKAAAPA 15  
Db 47 APAYSTYAAAVPA 60  
RESULT 5  
ID Q6YSU4 PRELIMINARY; PRT; 299 AA.  
AC Q6YSU4;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein P0680C01.22.  
GN Name=P0680C01.22;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
RT clone:P0680C01.";  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP006344; BAC84796.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 299 AA; 31850 MW; 4C14C4070BC31552 CRC64;  
Query Match 59.2%; Score 45; DB 2; Length 299;  
Best Local Similarity 73.3%; Pred. No. 32;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EAPKYEAYKAAAPA 15  
Db 262 EAPKVEATPAAATA 276  
RESULT 6  
QY 7S7R7  
ID Q7S7R7 PRELIMINARY; PRT; 408 AA.

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AC Q7S7R7;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, last annotation update)
DE Hypothetical protein (Probable translation elongation factor eEF-1,
DE gamma chain).
GN Name=NCU03826.1; Synonyms=82C3.020;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Reisman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-b(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000273; EAA31979.1; -.
DR EMBL; BX842617; CAE76104.1; -.
DR HSSP; P29547; 1NHX.
DR GO; GO:0005853; C:eukaryotic translation elongation factor 1. . .; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR001662; EFl_G.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR010987; GST_C_like.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00647; EFlG; 1.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR ProDom; PD006217; EFl_G; 1.
DR ProSITE; PS50040; EFlG; 1.
KW Elongation factor; Hypothetical protein.
SQ SEQUENCE 408 AA; 45741 MW; D5A8C7A3D1D6B178 CRC64;

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Query Match 59.2%; Score 45; DB 2; Length 408;
Best Local Similarity 73.3%; Pred. No. 43;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 EAPKYEAYKAAAPA 15
Db 222 EAPKPAAPKPAAPA 236

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RESULT 7
MLLF_MOUSE STANDARD; PRT; 192 AA.
ID MLEF_MOUSE
AC P09541;

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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Myosin light chain 1, atrial/fetal isoform (MLC1A) (MLC1EMB).
GN Name=Mlc1a; Synonyms=Myla;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=8315068; PubMed=2842339;
RA Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,
RA Buckingham M.E.;
RT "Structure and sequence of the myosin alkali light chain gene
RT expressed in adult cardiac atria and fetal striated muscle.";
RL J. Biol. Chem. 263:12669-12676(1988).
RN [2]
RP SEQUENCE OF 1-40 FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=89057447; PubMed=3194193;
RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
RA Buckingham M.E.;
RT "Promoter analysis of myosin alkali light chain genes expressed in
RT mouse striated muscle.";
RL Nucleic Acids Res. 16:10037-10052(1988).
CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
CC chains.
CC -1- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal
CC skeletal and ventricular muscle.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
CC PROTEIN DOES NOT BIND CALCIUM.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20772; AAA39721.1; -.
DR EMBL; M31017; AAA39721.1; JOINED.
DR EMBL; M20769; AAA39721.1; JOINED.
DR EMBL; M20770; AAA39721.1; JOINED.
DR EMBL; M20771; AAA39721.1; JOINED.
DR EMBL; X12971; CAA31414.1; -.
DR EMBL; M19436; AAA39720.1; -.
DR PIR; A31114; MOMS4E.
DR HSSP; P02607; 1BR1.
DR MGD; MGI:97267; Myla.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR ProDom; PD000012; EF-hand; 2.
KW Multigene family; Muscle protein; Myosin.
FT INIT MET 0
SQ SEQUENCE 192 AA; 21028 MW; B0439D512FA19C38 CRC64;

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Query Match 57.9%; Score 44; DB 1; Length 192;
Best Local Similarity 76.9%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 3 PKYEAYKAAAPA 15
Db 7 PKKEAAKPAAPA 19

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RESULT 8
Q6C9V2 PRELIMINARY; PRT; 316 AA.
ID Q6C9V2
AC Q6C9V2;
DT 25-OCT-2004 (Tremblrel. 28, Created)

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DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
DE 25-OCT-2004 (TReMBLrel. 28, last annotation update)
DE Similar to sp|P36110 Saccharomyces cerevisiae YKR013w PRY2
DE protein.
GN ORFNames=YAL10D08140g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382130; CAG80748.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PRD0837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; CRISP_1; 1.
SQ SEQUENCE 316 AA; 33458 MW; F88EDA9F938631B5 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 316;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
Db 126 EAPKQEAAPKSEAPS 140

RESULT 9
O73BN9 PRELIMINARY; PRT; 424 AA.
AC O73BN9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
DE 2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide
DE succinyltransferase (EC 2.3.1.61).
GN Name=odhB; OrderedLocuNames=BCE1379;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raske D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Foute D.E., Tourasse N.J., Angiolini S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic

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RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
DR EMBL; AE017268; AAS40308.1; -.
DR HSSP; P11961; 1B5S.
DR TIGR; BCE1379; -.
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR011053; Hybrid_motif.
DR InterPro; IPR003016; lipoyl_BS.
DR InterPro; IPR006255; SucB.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR PRODOM; PD001115; 2Oxoacid_dh; 1.
DR TIGRFAms; TIGR01347; sucB; 1.
DR PROSITE; PS00189; LIPOYL; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR ACyltransferase; Complete proteome; Lipoyl; Transferase.
KW SEQUENCE 424 AA; 45794 MW; B61F0CF90B78A54C CRC64;

Query Match 57.9%; Score 44; DB 2; Length 424;
Best Local Similarity 73.3%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAPKYEAYKAAAPA 15
Db 100 EAPKAEAPKAAAPSA 114

RESULT 10
Q869Y7 PRELIMINARY; PRT; 439 AA.
AC Q869Y7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Similar to Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
DE dihydrolipoamide succinyltransferase component of 2-oxoglutarate
DE dehydrogenase complex, mitochondrial (EC 2.3.1.61) (E2) (E2K).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.
DR EMBL; AC116305; AAO52267.1; -.
DR HSSP; P07016; 1C4T.
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

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DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
 DR InterPro; IPR001078; 2Oxoacid\_dh.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR011053; Hybrid\_motif.  
 DR InterPro; IPR003016; Lipoyl\_BS.  
 DR InterPro; IPR006255; SucB.  
 DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR ProDom; PD001115; 2Oxoacid\_dh; 1.  
 DR TIGRFAMs; TIGR01347; sucB; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 KW Acyltransferase; Lipoyl; Transferase.  
 SQ SEQUENCE 439 AA; 4763 MW; 214DE063A7139A79 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 439;  
 Best Local Similarity 76.9%; Pred. No. 68;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 APKYEAYKAAAP 14  
 ||| ||| ||| |||  
 Db 155 APKVEAPKAAEAP 167

RESULT 11  
 Q7WJF6 PRELIMINARY; PRT; 591 AA.

AC Q7WJF6; 01-OCT-2003 (TReMBLrel. 25, Created)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Dihydrolipoamide dehydrogenase (EC 1.8.1.4).  
 GN Name=IpdA; Synonyms=Ipd; OrderedLocustNames=BB2538;  
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RB50 / ATCC BAA-588;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdano-Tarrega A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsis K.,  
 RA Leather S., Moule S., Norbertzak H., O'Neil S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens K.,  
 RA Unwin I., Whitehead S., Barrett B.G., Maskell D.J.,  
 RA "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
 DR EMBL; BX640444; CAB33032.1; -.  
 DR HSSP; Q51225; 1BHY.  
 DR GO; GO:0005737; C:Cytoplasm; IEA.  
 DR GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IEA.  
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR001327; FAD\_pyr\_redox.  
 DR InterPro; IPR011053; Hybrid\_motif.  
 DR InterPro; IPR006258; lipamide\_dh.  
 DR InterPro; IPR003016; lipoyl\_BS.  
 DR InterPro; IPR001100; Pyr\_redox.  
 DR InterPro; IPR004099; Pyr\_redox\_dim.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF00070; Pyr\_redox; 1.  
 DR Pfam; PF02852; Pyr\_redox\_dim; 1.  
 DR ProDom; PD000139; FAD\_pyr\_redox; 1.

DR TIGRFAMs; TIGR01350; lipamide\_DH; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 DR PROSITE; PS00076; PYRIDINE\_REDOX\_1; 1.  
 KW Complete proteome; Lipoyl; Oxidoreductase.  
 SQ SEQUENCE 591 AA; 61923 MW; 1DA641207AD41D47 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 591;  
 Best Local Similarity 73.3%; Pred. No. 90;  
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAPKYEAYKAAAP 15  
 ||| ||| ||| |||  
 Db 95 EAPKAEAPKAPAKA 109

RESULT 12

O8H1Y7 PRELIMINARY; PRT; 802 AA.

AC O8H1Y7; 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Starch synthase II.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,  
 RA Rampling L., Kosar-Harshemi B., Rahman S., Morell M.K.;  
 RT "The structural organization of the gene encoding class II starch  
 RT synthase of wheat and barley, and the evolution of the genes encoding  
 RT starch synthases in plants.";  
 RL Funct. Integr. Genomics 0:0-0(2002).  
 DR EMBL; AY133251; AAN28307.1; -.  
 DR EMBL; AY133250; AAN28307.1; JOINED.  
 DR GO; GO:0009058; P:biosynthesis; IEA.  
 SQ SEQUENCE 802 AA; 87473 MW; 9F7649133F81BE51 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 802;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EAPKYEAYKAAAP 15  
 ||| ||| ||| |||  
 Db 246 EAPKPKALISAPAPA 260

RESULT 13

O8H1Y8 PRELIMINARY; PRT; 802 AA.

AC O8H1Y8; 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Starch synthase II.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,  
 RA Rampling L., Kosar-Harshemi B., Rahman S., Morell M.K.;  
 RT "The structural organization of the gene encoding class II starch  
 RT synthase of wheat and barley, and the evolution of the genes encoding  
 RT starch synthases in plants.";  
 RL Funct. Integr. Genomics 0:0-0(2002).  
 DR EMBL; AY133249; AAN28309.1; -.  
 DR GO; GO:0009058; P:biosynthesis; IEA.



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 76.6837 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-65

Perfect score: 71

Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	71	100.0	15	5	ABP52271	Abp52271 HLA-DR2 m
2	71	100.0	15	5	ABP52298	Abp52298 HLA-DR2 m
3	71	100.0	17	5	ABP52294	Abp52294 HLA-DR2 m
4	71	100.0	17	5	ABP52296	Abp52296 HLA-DR2 m
5	71	100.0	19	5	ABP52295	Abp52295 HLA-DR2 m
6	65	91.5	15	5	ABP52270	Abp52270 HLA-DR2 m
7	63	88.7	15	5	ABP52301	Abp52301 HLA-DR2 m
8	62	87.3	17	5	ABP52303	Abp52303 HLA-DR2 m
9	61	85.9	15	5	ABP52291	Abp52291 HLA-DR2 m
10	61	85.9	15	5	ABP52263	Abp52263 HLA-DR2 m
11	60	84.5	15	5	ABP52272	Abp52272 HLA-DR2 m
12	59	83.1	15	5	ABP52259	Abp52259 HLA-DR2 m
13	59	83.1	15	5	ABP52257	Abp52257 HLA-DR2 m
14	58	81.7	17	5	ABP52302	Abp52302 HLA-DR2 m
15	57	80.3	15	5	ABP52297	Abp52297 HLA-DR2 m
16	56	78.9	15	5	ABP52253	Abp52253 HLA-DR2 m
17	56	78.9	15	5	ABP52251	Abp52251 HLA-DR2 m
18	56	78.9	15	5	ABP52239	Abp52239 HLA-DR2 m
19	55	77.5	15	5	ABP52290	Abp52290 HLA-DR2 m
20	55	77.5	15	5	ABP52261	Abp52261 HLA-DR2 m
21	55	77.5	15	5	ABP52244	Abp52244 HLA-DR2 m
22	55	77.5	15	5	ABP52292	Abp52292 HLA-DR2 m
23	55	77.5	15	5	ABP52269	Abp52269 HLA-DR2 m
24	55	77.5	15	5	ABP52262	Abp52262 HLA-DR2 m
25	54	76.1	15	5	ABP52264	Abp52264 HLA-DR2 m

26	54	76.1	15	5	ABP52267	Abp52267 HLA-DR2 m
27	54	76.1	15	5	ABP52236	Abp52236 HLA-DR2 m
28	53	74.6	15	5	ABP52299	Abp52299 HLA-DR2 m
29	52	73.2	15	5	ABP52265	Abp52265 HLA-DR2 m
30	51	71.8	15	5	ABP52254	Abp52254 HLA-DR2 m
31	51	71.8	15	5	ABP52255	Abp52255 HLA-DR2 m
32	51	71.8	15	5	ABP52240	Abp52240 HLA-DR2 m
33	51	71.8	15	5	ABP52241	Abp52241 HLA-DR2 m
34	51	71.8	15	5	ABP52304	Abp52304 HLA-DR2 m
35	51	71.8	15	5	ABP52248	Abp52248 HLA-DR2 m
36	51	71.8	15	5	ABP52249	Abp52249 HLA-DR2 m
37	50	70.4	15	5	ABP52232	Abp52232 HLA-DR2 m
38	50	70.4	15	5	ABP52268	Abp52268 HLA-DR2 m
39	50	70.4	15	5	ABP52231	Abp52231 HLA-DR2 m
40	49	69.0	15	5	ABP52250	Abp52250 HLA-DR2 m
41	49	69.0	15	5	ABP52277	Abp52277 HLA-DR2 m
42	48	67.6	15	5	ABP52238	Abp52238 HLA-DR2 m
43	48	67.6	15	5	ABP52243	Abp52243 HLA-DR2 m
44	48	67.6	15	5	ABP52280	Abp52280 HLA-DR2 m
45	48	67.6	15	5	ABP52280	Abp52280 HLA-DR2 m

ALIGNMENTS

RESULT 1  
ABP52271  
ID ABP52271 standard; peptide; 15 AA.  
XX  
AC ABP52271;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M,  
XX WPI; 2002-608439/65.  
XX  
XX  
XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX residues. The complex of the peptide with a major histocompatibility  
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an  
XX immune response. (I) has antiinflammatory and neuroprotective activities,  
XX and can be used as a MHC class II protein inhibitor. The compositions  
XX comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
DB 1 EKAKYEAYKAAAAA 15  
RESULT 2  
ABP52298  
ID ABP52298 standard; peptide; 15 AA.  
XX  
AC ABP52298;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 15 AA;  
Query Match 100.0%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
DB 1 EKAKYEAYKAAAAA 15  
RESULT 3  
ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
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CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 71; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15

DB 3 EKAKYEAYKAAAAA 17

RESULT 4

ID ABP52296 standard; peptide; 17 AA.

AC ABP52296;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:90.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 17 AA;

Query Match 100.0%; Score 71; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
ID 1 EKAKYEAYKAAAAA 15

RESULT 5  
ABP52295  
ID ABP52295 standard; peptide; 19 AA.

XX ABP52295;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:89.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 19 AA;

Query Match 100.0%; Score 71; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
DB 3 EKAKYEAYKAAAAA 17

RESULT 6  
ABP52270  
ID ABP52270 standard; peptide; 15 AA.  
AC ABP52270;  
XX 16-OCT-2002 (first entry)  
DT HLA-DR2 molecule binding peptide SEQ ID NO:64.  
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 91.5%; Score 65; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00054;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 EKAKEYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAKKFEAFKAAAAA 15  
| | | | | | | | | | | | | | |  
RESULT 7  
ABP52301  
ID ABP52301 standard; peptide, 15 AA.  
XX  
AC ABP52301;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:95.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 88.7%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0012;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EKAKEYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAKKFEAFKAAAAA 15  
| | | | | | | | | | | | | | |  
RESULT 8  
ABP52303  
ID ABP52303 standard; peptide, 17 AA.  
XX  
AC ABP52303;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 87.3%; Score 62; DB 5; Length 17;  
Best Local Similarity 86.7%; Pred. No. 0.0019;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 EKAKYEAYKAAAAA 15  
|||:|||||||  
DB 3 EKAKFEAYKAAAAA 17  
RESULT 9  
ABP52291  
ID ABP52291 standard; peptide; 15 AA.  
XX  
XX ABP52291;  
AC  
XX 16-OCT-2002 (first entry)  
DT  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200259143-A2.  
PN  
XX  
PD 01-AUG-2002.  
PD  
PF 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Strominger JL, Fridkis-Hareli M;  
PI

XX  
DR WPI; 2002-608439/65.  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 85.9%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0025;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 EKAKYEAYKAAAAA 15  
|||:|||||||  
DB 1 EKPKYEAYKAAAAA 15  
RESULT 10  
ABP52263  
ID ABP52263 standard; peptide; 15 AA.  
XX  
XX ABP52263;  
AC  
XX  
DT 16-OCT-2002 (first entry)  
DT  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:57.  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200259143-A2.  
PN  
XX  
PD 01-AUG-2002.  
PD  
PF 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX WPI; 2002-608439/65.  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
PT

```
XX Example 1; Page 33; 54pp; English.
PS
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
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CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match      85.9%; Score 61; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 EKAKEYEAYKAAAAA 15
        |:||| ||||| |||
Db       1 EAKYAAAYKAAAAA 15

RESULT 11
ABP52272 ID ABP52272 standard; peptide; 15 AA.
XX
AC ABP52272;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:66.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
```

```
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match      84.5%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 EKAKEYEAYKAAAAA 15
        |:||| ||||| |||
Db       1 EAKYEAAYKAAAAA 15

RESULT 12
ABP52259 ID ABP52259 standard; peptide; 15 AA.
XX
AC ABP52259;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:53.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 83.1%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0053;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EKAKEYEAYKAAAAA 15  
DB 1 EKAAYAAAYKAAAAA 15  
RESULT 13  
ABP52257  
ID ABP52257 standard; peptide; 15 AA.  
XX  
AC ABP52257;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 32; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents, and a side effect of administering an anti-  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 83.1%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0053;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EKAKEYEAYKAAAAA 15  
DB 1 EKAAYAAAYKAAAAA 15  
RESULT 14  
ABP52302  
ID ABP52302 standard; peptide; 17 AA.  
XX  
AC ABP52302;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
Query Match 81.7%; Score 58; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0089;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EKAKEYEAYKAAAAA 15  
DB 3 EKAKEYEAYKAAAAA 17

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RESULT 15
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

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Query Match 80.3%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 EKAKYEAYKAAAAA 15
Db 1 EKPKEAYKAAAPA 15

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Search completed: February 26, 2005, 23:48:21  
Job time : 79.6837 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 20.051 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-65  
Perfect score: 71  
Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	59.2	13	5 PCT-US95-04121-38	Sequence 38, Appl
2	42	59.2	1001	4 US-09-248-796A-18658	Sequence 18658, A
3	41	57.7	402	4 US-09-248-796A-17859	Sequence 17859, A
4	40	56.3	13	5 PCT-US94-10257A-33	Sequence 33, Appl
5	40	56.3	109	4 US-09-405-743A-7	Sequence 7, Appl
6	40	56.3	109	4 US-09-816-989A-7	Sequence 7, Appl
7	40	56.3	466	4 US-09-489-039A-13950	Sequence 13950, A
8	40	56.3	1156	4 US-09-198-452A-171	Sequence 171, App
9	40	56.3	1562	4 US-09-438-185A-152	Sequence 152, App
10	39	54.9	497	1 US-08-295-670-6	Sequence 6, Appl
11	39	54.9	497	1 US-08-633-485-6	Sequence 6, Appl
12	39	54.9	510	3 US-08-508-761B-4	Sequence 4, Appl
13	39	54.9	601	4 US-09-252-991A-21824	Sequence 21824, A
14	39	54.9	731	4 US-09-252-991A-18769	Sequence 18769, A
15	38	53.5	186	4 US-09-902-540-11242	Sequence 11242, A
16	38	53.5	576	4 US-09-543-681A-7747	Sequence 7747, Ap
17	38	53.5	582	4 US-09-919-497-100	Sequence 100, App
18	38	53.5	759	4 US-09-328-352-4241	Sequence 4241, Ap
19	37.5	52.8	391	4 US-09-902-540-11110	Sequence 11110, A
20	37	52.1	38	3 US-09-117-121-16	Sequence 16, Appl
21	37	52.1	38	3 US-09-117-121-24	Sequence 24, Appl
22	37	52.1	38	4 US-09-344-529-5	Sequence 5, Appl
23	37	52.1	56	4 US-09-405-743A-3	Sequence 3, Appl
24	37	52.1	56	4 US-09-816-989A-3	Sequence 3, Appl
25	37	52.1	77	4 US-09-405-743A-5	Sequence 5, Appl
26	37	52.1	77	4 US-09-816-989A-5	Sequence 5, Appl
27	37	52.1	86	4 US-09-405-743A-6	Sequence 6, Appl

28	37	52.1	86	4	US-09-816-989A-6	Sequence 6, Appl
29	37	52.1	143	4	US-09-270-767-33766	Sequence 33766, A
30	37	52.1	143	4	US-09-270-767-48983	Sequence 48983, A
31	37	52.1	459	4	US-09-543-681A-5116	Sequence 5116, Ap
32	37	52.1	596	2	US-08-836-620A-16	Sequence 16, Appl
33	37	52.1	615	4	US-09-902-540-10642	Sequence 10642, A
34	37	52.1	802	4	US-09-489-039A-11230	Sequence 11230, A
35	37	52.1	958	1	US-08-426-236-4	Sequence 4, Appl
36	36.5	51.4	45	4	US-09-405-743A-2	Sequence 2, Appl
37	36.5	51.4	45	4	US-09-816-989A-2	Sequence 2, Appl
38	36	50.7	13	5	PCT-US95-04121-60	Sequence 30, Appl
39	36	50.7	54	3	US-09-117-121-30	Sequence 60, Appl
40	36	50.7	166	4	US-09-252-991A-22139	Sequence 22139, A
41	36	50.7	180	6	5273901-7	Patent No. 5273901
42	36	50.7	180	6	5482709-6	Patent No. 5482709
43	36	50.7	180	6	5273901-7	Patent No. 5273901
44	36	50.7	180	6	5482709-6	Patent No. 5482709
45	36	50.7	209	4	US-09-489-039A-12638	Sequence 12638, A

## ALIGNMENTS

RESULT 1  
PCT-US95-04121-38  
; Sequence 38, Application PC/TUS9504121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof  
; NUMBER OF SEQUENCES: 62  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222,206  
; FILING DATE: April 1, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vanstone, Darlene A.  
; REGISTRATION NUMBER: 35,279  
; REFERENCE/DOCKET NUMBER: 079.2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6010  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; PCT-US95-04121-38

Query Match 59.2%; Score 42; DB 5; Length 13;  
Best Local Similarity 76.9%; Pred. No. 0.92;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 15  
Db 1 AAYKAAKAAAAA 13

RESULT 2  
US-09-248-796A-18658  
; Sequence 18658, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
PRIOR FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 18658  
LENGTH: 1001  
TYPE: PRT  
ORGANISM: Candida albicans  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (21)  
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno  
US-09-248-796A-18658

Query Match 59.2%; Score 42; DB 4; Length 1001;  
Best Local Similarity 78.6%; Pred. No. 78;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 KAKYEAYKAAAAA 15  
Db 818 KAKEEABAAAAAAA 831

RESULT 3  
US-09-248-796A-17859  
Sequence 17859, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 17859  
LENGTH: 402  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-17859

Query Match 57.7%; Score 41; DB 4; Length 402;  
Best Local Similarity 80.0%; Pred. No. 45;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KAKYEAYKAA 11  
Db 70 KAKYESYDAA 79

RESULT 4  
PCT-US94-10257A-33  
Sequence 33, Application PC/TUS9410257A  
GENERAL INFORMATION:  
APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION  
APPLICANT: BRIGITTE DEVAUX  
APPLICANT: JONATHAN B. ROTHBARD  
APPLICANT: DAWN SMILEK  
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE  
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS  
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE  
NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10257A  
FILING DATE: 1 SEPTEMBER 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,824  
FILING DATE: 03-SEP-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ANNE I CRAIG  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 071.1 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-10257A-33

Query Match 56.3%; Score 40; DB 5; Length 13;  
Best Local Similarity 76.9%; Pred. No. 1.9;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 AKYEAYKAAAAA 15  
Db 1 AAYAAAKAAAAA 13

RESULT 5  
US-09-405-743A-7  
Sequence 7, Application US/09405743A  
Patent No. 6514938  
GENERAL INFORMATION:  
APPLICANT: Yeda Research and Development Co., Ltd.  
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
FILE REFERENCE: 60807-A  
CURRENT APPLICATION NUMBER: US/09/405,743A  
CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
OTHER INFORMATION: PEPTIDE  
US-09-405-743A-7

Query Match 56.3%; Score 40; DB 4; Length 109;  
Best Local Similarity 81.8%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KAKYEAYKAAA 12  
Db 55 KAKKEAYKAAE 65

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RESULT 6
US-09-816-989A-7
; Sequence 7, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-7

Query Match          56.3%; Score 40; DB 4; Length 109;
Best Local Similarity 81.8%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAKYEAYKAAA 12
||| |||||
DB 55 KAKKEAYKAAE 65

RESULT 7
US-09-489-039A-13950
; Sequence 13950, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13950
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950

Query Match          56.3%; Score 40; DB 4; Length 466;
Best Local Similarity 76.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 15
| || |||||
DB 153 ASLEAQKAAAAA 165

RESULT 8
US-09-198-452A-171
; Sequence 171, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffaïs, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
```

```
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 171
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-171

Query Match          56.3%; Score 40; DB 4; Length 1156;
Best Local Similarity 64.3%; Pred. No. 1.9e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKEAYKAAAA 14
||: ||: |||
DB 659 EKSKYDNEKAAAA 672

RESULT 9
US-09-438-185A-152
; Sequence 152, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Kalman, Sue
; APPLICANT: Mitchell, Wayne
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 1562
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0150
US-09-438-185A-152

Query Match          56.3%; Score 40; DB 4; Length 1562;
Best Local Similarity 64.3%; Pred. No. 2.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKEAYKAAAA 14
||: ||: |||
DB 1065 EKSKYDNEKAAAA 1078

RESULT 10
US-08-295-670-6
; Sequence 6, Application US/08295670
; Patent No. 5547864
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: MIWA, KIYOSHI
; APPLICANT: KAWAHARA, YOSHIO
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
```

STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,670  
FILING DATE: 08-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/00039  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-4069  
FILING DATE: 13-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5547864man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-697-0 PCT  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-295-670-6

Query Match 54.9%; Score 39; DB 1; Length 497;  
Best Local Similarity 53.3%; Pred. No. 1.2e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15  
Db 104 EQAAYEAFEARVR 118

RESULT 11  
US-08-633-485-6  
Sequence 6, Application US/08633485  
Patent No. 5681717  
GENERAL INFORMATION:  
APPLICANT: KAWASAKI, HISASHI  
APPLICANT: TSUCHIYA, MAKOTO  
APPLICANT: MIWA, KIYOSHI  
APPLICANT: KAWAHARA, YOSHIO  
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,485  
FILING DATE: 17-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/295,670

FILING DATE: 08-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00039  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-4069  
FILING DATE: 13-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5681717man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-697-0 PCT  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-633-485-6

Query Match 54.9%; Score 39; DB 1; Length 497;  
Best Local Similarity 53.3%; Pred. No. 1.2e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15  
Db 104 EQAAYEAFEARVR 118

RESULT 12  
US-08-508-761B-4  
Sequence 4, Application US/08508761B  
Patent No. 6027920  
GENERAL INFORMATION:  
APPLICANT: Joliff, Gwennael  
APPLICANT: Guyonvarch, Arnel  
APPLICANT: Purification, Relano  
APPLICANT: Duchillon, Francis  
APPLICANT: Renaud, Michel  
TITLE OF INVENTION: System for Protein Expression and  
TITLE OF INVENTION: Secretion Especially in Corynebacteria  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,761B  
FILING DATE: 31-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91/09652  
FILING DATE: 29-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91/09870  
FILING DATE: 02-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: P58525NA  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 510 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-508-761B-4

Query Match 54.9%; Score 39; DB 3; Length 510;  
Best Local Similarity 53.3%; Pred. No. 1.2e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15  
DB 104 EQAAYEAFEAARVRA 118

## RESULT 13

US-09-252-991A-21824  
Sequence 21824, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21824  
LENGTH: 601  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (601)  
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-21824

Query Match 54.9%; Score 39; DB 4; Length 601;  
Best Local Similarity 58.3%; Pred. No. 1.4e+02;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 14  
DB 570 ARYEAYRSAIVA 581

## RESULT 14

US-09-252-991A-18769  
Sequence 18769, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18769  
LENGTH: 731  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18769

Query Match 54.9%; Score 39; DB 4; Length 731;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAA 15  
DB 179 YEAYEACACARA 189

## RESULT 15

US-09-902-540-11242  
Sequence 11242, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 11242  
LENGTH: 186  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-11242

Query Match 53.5%; Score 38; DB 4; Length 186;  
Best Local Similarity 66.7%; Pred. No. 62;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 14  
DB 49 ASYQYKAAADA 60

Search completed: February 26, 2005, 23:59:27  
Job time : 22.051 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 53.5714 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-65  
Perfect score: 71  
Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	15	14	US-10-056-583-65 Sequence 65, Appl
2	71	100.0	17	14	US-10-056-583-88 Sequence 88, Appl
3	71	100.0	17	14	US-10-056-583-90 Sequence 90, Appl
4	71	100.0	19	14	US-10-056-583-89 Sequence 89, Appl
5	65	91.5	15	14	US-10-056-583-64 Sequence 64, Appl
6	63	88.7	15	14	US-10-056-583-95 Sequence 95, Appl
7	62	87.3	15	14	US-10-056-583-92 Sequence 92, Appl
8	62	87.3	17	14	US-10-056-583-97 Sequence 97, Appl
9	61	85.9	15	14	US-10-056-583-57 Sequence 57, Appl
10	61	85.9	15	14	US-10-056-583-85 Sequence 85, Appl
11	60	84.5	15	14	US-10-056-583-66 Sequence 66, Appl
12	59	83.1	15	14	US-10-056-583-51 Sequence 51, Appl
13	59	83.1	15	14	US-10-056-583-53 Sequence 53, Appl

	14	58	81.7	17	14	US-10-056-583-96	Sequence 96, Appl
15	57	80.3	15	14	US-10-056-583-91	Sequence 91, Appl	
16	56	78.9	15	14	US-10-056-583-33	Sequence 33, Appl	
17	56	78.9	15	14	US-10-056-583-45	Sequence 45, Appl	
18	56	78.9	15	14	US-10-056-583-47	Sequence 47, Appl	
19	55	77.5	15	14	US-10-056-583-38	Sequence 38, Appl	
20	55	77.5	15	14	US-10-056-583-55	Sequence 55, Appl	
21	55	77.5	15	14	US-10-056-583-56	Sequence 56, Appl	
22	55	77.5	15	14	US-10-056-583-63	Sequence 63, Appl	
23	55	77.5	15	14	US-10-056-583-84	Sequence 84, Appl	
24	55	77.5	15	14	US-10-056-583-86	Sequence 86, Appl	
25	54	76.1	15	14	US-10-056-583-58	Sequence 58, Appl	
26	54	76.1	15	14	US-10-056-583-30	Sequence 30, Appl	
27	54	76.1	15	14	US-10-056-583-61	Sequence 61, Appl	
28	53	74.6	15	14	US-10-056-583-93	Sequence 93, Appl	
29	52	73.2	15	14	US-10-056-583-59	Sequence 59, Appl	
30	51	71.8	15	14	US-10-056-583-34	Sequence 34, Appl	
31	51	71.8	15	14	US-10-056-583-35	Sequence 35, Appl	
32	51	71.8	15	14	US-10-056-583-42	Sequence 42, Appl	
33	51	71.8	15	14	US-10-056-583-43	Sequence 43, Appl	
34	51	71.8	15	14	US-10-056-583-48	Sequence 48, Appl	
35	51	71.8	15	14	US-10-056-583-49	Sequence 49, Appl	
36	51	71.8	15	14	US-10-056-583-98	Sequence 98, Appl	
37	50	70.4	15	14	US-10-056-583-25	Sequence 25, Appl	
38	50	70.4	15	14	US-10-056-583-26	Sequence 26, Appl	
39	50	70.4	15	14	US-10-056-583-62	Sequence 62, Appl	
40	49	69.0	15	14	US-10-056-583-29	Sequence 29, Appl	
41	49	69.0	15	14	US-10-056-583-44	Sequence 44, Appl	
42	48	67.6	15	14	US-10-056-583-32	Sequence 32, Appl	
43	48	67.6	15	14	US-10-056-583-37	Sequence 37, Appl	
44	48	67.6	15	14	US-10-056-583-39	Sequence 39, Appl	
45	48	67.6	15	14	US-10-056-583-52	Sequence 52, Appl	

## ALIGNMENTS

RESULT 1  
US-10-056-583-65  
; Sequence 65, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056, 583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263, 569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-65

Query Match 100.0%; Score 71; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15  
Db 1 EKAKYEAYKAAAAA 15

RESULT 2  
US-10-056-583-88

```
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

```
Query Match          100.0%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAA 15
        |||||||
Db      3 EKAKYEAYKAAAAA 17
```

```
RESULT 3
US-10-056-583-90;
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match          100.0%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAA 15
        |||||||
Db      1 EKAKYEAYKAAAAA 15
```

```
RESULT 4
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match          100.0%; Score 71; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAA 15
        |||||||
Db      3 EKAKYEAYKAAAAA 17
```

```
RESULT 5
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match          91.5%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00074;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAA 15
        |||||||
Db      1 EAAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95
```

```
Query Match      88.7%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYEAYKAAAAA 15
         ||||:|||||
Db       1 EKAKEEAFKAAAAA 15
```

```
RESULT 7
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92
```

```
Query Match      87.3%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0022;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYEAYKAAAAA 15
         ||||:|||||
Db       1 EKAKEEAYKAAAAA 15
```

```
RESULT 8
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match      87.3%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYEAYKAAAAA 15
         ||||:|||||
Db       3 EKAKEEAYKAAAAA 17
```

```
RESULT 9
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57
```

```
Query Match      85.9%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0032;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKEYEAYKAAAAA 15
         ||||:|||||
Db       1 EAKYAAAYKAAAAA 15
```

```
RESULT 10
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-85

Query Match 85.9%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0032;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
|||  
Db 1 EKPKYEAYKAAAAA 15

RESULT 11  
US-10-056-583-66

; Sequence 66, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 84.5%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0047;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
|||  
Db 1 EAKKYEAYKAAAAA 15

RESULT 12  
US-10-056-583-51

; Sequence 51, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 83.1%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0067;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
|||  
Db 1 EAKKYEAYKAAAAA 15

RESULT 13  
US-10-056-583-53

; Sequence 53, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-53

Query Match 83.1%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0067;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
|||  
Db 1 EAKKYEAYKAAAAA 15

RESULT 14  
US-10-056-583-96

; Sequence 96, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-96

Query Match 81.7%; Score 58; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.011;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
|||  
Db 3 EAKKFEAYKAAAAA 17

RESULT 15

US-10-056-583-91

; Sequence 91, Application US/10056583  
; Publication No. US20030064915A1

; GENERAL INFORMATION:

; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/10/056,583

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 91

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-91

Query Match 80.3%; Score 57; DB 14; Length 15;

Best Local Similarity 80.0%; Pred. No. 0.014;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKYEAYKAAAAA 15

Db 1 EKPKFEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:22  
Job time : 54.5714 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 / Search time 13.3163 Seconds  
(without alignments)  
108.382 Million cell updates/sec

Title: US-10-056-583A-65  
Perfect score: 71  
Sequence: 1 EKAKYEAYKRAAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	60.6	185	2	S36290 T-cell receptor ga
2	42	59.2	179	2	F97683 50S ribosomal prot
3	42	59.2	179	2	AF2908 50S ribosomal prot
4	42	59.2	188	2	I50145 homeotic protein H
5	42	59.2	289	2	A43562 homeotic protein H
6	41.5	58.5	189	2	S77930 exoskeletal protei
7	41.5	58.5	189	2	S77935 exoskeletal protei
8	41	57.7	177	2	AD1307 peptidyl methionin
9	41	57.7	177	2	AD1679 peptidyl methionin
10	41	57.7	254	2	H86355 peptidyl methionin
11	41	57.7	1885	1	JC4086 fatty-acid synthas
12	41	57.7	2129	2	T27431 fatty-acid synthas
13	40	56.3	73	2	S40015 phd protein - phag
14	40	56.3	377	2	T43037 probable fatty-aci
15	40	56.3	421	2	JV0057 tola protein - Esc
16	40	56.3	478	2	S04675 H+-transporting tw
17	40	56.3	806	2	T13690 hypothetical prote
18	40	56.3	1537	2	F86509 CT147 hypothetical
19	40	56.3	1537	2	C81558 conserved hypothet
20	40	56.3	1537	2	H72112 ct147 hypothetical
21	40	56.3	1842	2	T43409 probable fatty-aci
22	40	56.3	1842	2	T38781 fatty acid synthas
23	39	54.9	113	2	T30041 hypothetical prote
24	39	54.9	250	2	T51971 proteasome endopep
25	39	54.9	318	2	B48487 Moch (Tr4399) - Ba
26	39	54.9	436	2	T31902 hypothetical prote
27	39	54.9	510	2	S35028 protein P82 precur
28	39	54.9	553	2	D83640 hypothetical prote
29	39	54.9	698	2	T32594 hypothetical prote

30	39	54.9	728	2	H82965 DNA helicase II PA
31	39	54.9	1430	2	T34516 hypothetical prote
32	39	54.9	2957	2	T33152 hypothetical prote
33	38	53.5	101	2	G75512 conserved hypothet
34	38	53.5	108	2	F97521 VCO3 protein homo
35	38	53.5	108	2	AH2740 conserved hypothet
36	38	53.5	140	2	D81970 H+-transporting tw
37	38	53.5	159	2	A97836 hypothetical prote
38	38	53.5	170	2	E81312 probable lipoprote
39	38	53.5	178	2	S03216 hypothetical prote
40	38	53.5	289	2	AC1399 hypothetical prote
41	38	53.5	346	2	C82156 conserved hypothet
42	38	53.5	368	2	B82357 conserved hypothet
43	38	53.5	398	2	T21061 hypothetical prote
44	38	53.5	433	2	D87408 ATPase, AAA family
45	38	53.5	478	2	E87470 efflux system prot

ALIGNMENTS

RESULT 1

S36290  
T-cell receptor gamma chain precursor - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C/Accession: S36290; S23041  
R/Hein, W.R.; Dudler, L.  
EMBO J. 12, 715-724, 1993  
A/Title: Divergent evolution of T cell repertoires: extensive diversity and development  
A/Reference number: S36287; MUID:93178447; PMID:8440261  
A/Accession: S36290  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-185 <HEI>  
A/Cross-references: EMBL:Z12998; NID:G2260; PIDN:CAA78342.1; PID:G2261  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match

Best Local Similarity 60.6%; Score 43; DB 2; Length 185;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAYKRAA 12

Db 81 DKAKYSVYKGA 92

RESULT 2

F97683  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97683  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97683  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK8423.1; PID:g15157917; GSPDB: C/Genetics:  
A/Gene: AGR\_C\_4900  
A/Map position: circular chromosome  
C/Superfamily: Escherichia coli ribosomal protein L19

Query Match

Best Local Similarity 59.2%; Score 42; DB 2; Length 179;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKAKYEAYKAAAAA 15  
|||: ||| |||  
Db 137 EKARLEAEKVAQA 151

## RESULT 3

AF2908

50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: AF2908

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577, MUID:21608550; PMID:11743193

A:Accession: AF2908

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-179 &lt;XUR&gt;

A:Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: rplS

A:Map position: circular chromosome

C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 59.2%; Score 42; DB 2; Length 179;  
Best Local Similarity 66.7%; Pred. No. 9.7;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKAKYEAYKAAAAA 15  
|||: ||| |||  
Db 137 EKARLEAEKVAQA 151

## RESULT 4

I50145

homeotic protein Hox M - chicken

N:Alternate names: CHOX M

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004

C:Accession: I50145; S14512

R:Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.

Leukemia 5, 357-360, 1991

A:Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viru

A:Reference number: I50145; MUID:91238215; PMID:1674560

A:Accession: I50145

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-188 &lt;CRO&gt;

A:Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701

C:Genetics:

A:Gene: CHOX M

C:Superfamily: homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:96-152/Domain: homeobox homology &lt;HOX&gt;

Query Match 59.2%; Score 42; DB 2; Length 188;  
Best Local Similarity 81.8%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 YEAYKAAAAA 15  
| ||| |||  
Db 10 YSKYKAAAAA 20

## RESULT 5

A43562

homeotic protein Hox D8 - mouse

N:Alternate names: homeotic protein Hox 4.3

C:Species: Mus musculus (house mouse)

C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004

C:Accession: A43562

R:Izpisua-Belmonte, J.C.; Dollé, P.; Renucci, A.; Zapavigna, V.; Falkenstein, H.; Dubo

Development 110, 733-745, 1990

A:Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob

A:Reference number: A43562; MUID:91209232; PMID:1982431

A:Accession: A43562

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-289 &lt;IZP&gt;

A:Cross-references: UNIPROT:P23463

C:Superfamily: homeotic protein Hox A7; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:196-252/Domain: homeobox homology &lt;HOX&gt;

Query Match 59.2%; Score 42; DB 2; Length 289;  
Best Local Similarity 81.8%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 YEAYKAAAAA 15  
| ||| |||  
Db 10 YSKYKAAAAA 20

## RESULT 6

S77930

exoskeletal protein HACP202A - American lobster (fragment)

C:Species: Homarus americanus (American lobster)

C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004

C:Accession: S77930

R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.

submitted to the Protein Sequence Database, June 1997

A:Description: Characterization of exoskeletal proteins from the American lobster, Homa

A:Reference number: S77925

A:Accession: S77930

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-189 &lt;NOU&gt;

A:Cross-references: UNIPROT:Q7M496

Query Match 58.5%; Score 41.5; DB 2; Length 189;  
Best Local Similarity 62.5%; Pred. No. 12;  
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Oy 1 EKAK-YEAYKAAAAA 15  
|||: ::||| |||  
Db 11 EKARFFQAFKAAEAAA 26

## RESULT 7

S77935

exoskeletal protein HACP202B - American lobster (fragment)

C:Species: Homarus americanus (American lobster)

C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004

C:Accession: S77935

R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.

submitted to the Protein Sequence Database, June 1997

A:Description: Characterization of exoskeletal proteins from the American lobster, Homa

A:Reference number: S77925

A:Accession: S77935

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-189 &lt;NOU&gt;

A:Cross-references: UNIPROT:Q7M495

Query Match 58.5%; Score 41.5; DB 2; Length 189;  
Best Local Similarity 62.5%; Pred. No. 12;  
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Oy 1 EKAK-YEAYKAAAAA 15  
|||: ::||| |||

Db 11 EKARFFQAFKAAEAAA 26

RESULT 8

AD1307

peptidyl methionine sulfoxide reductases homolog lmo1860 [imported] - Listeria monocytog

C/Species: Listeria monocytogenes

C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AD1307

R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlard,  
A/Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AD1307

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-177 <GLA>

A/Cross-references: UNIPROT:Q8Y640; GB:NC\_003210; PIDN:CAC99938.1; PID:g16411314; GSPDB:  
A/Experimental source: strain EGD-e

C/Genetics:

A/Gene: lmo1860

C/Superfamily: peptide methionine sulfoxide reductase

Query Match 57.7%; Score 41; DB 2; Length 177;  
Best Local Similarity 53.3%; Pred. No. 14;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15

Db 154 EKAHYEGYQVASGRA 168

RESULT 9

AD1679

peptidyl methionine sulfoxide reductases homolog lin1974 [imported] - Listeria innocua

C/Species: Listeria innocua

C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AD1679

R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001

A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlard,  
A/Title: Comparative genomics of Listeria species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AD1679

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-177 <GLA>

A/Cross-references: UNIPROT:Q92AE8; GB:AL592022; PIDN:CAC97204.1; PID:g16414475; GSPDB:  
A/Experimental source: strain Clj11262

C/Genetics:

A/Gene: lin1974

C/Superfamily: peptide methionine sulfoxide reductase

Query Match 57.7%; Score 41; DB 2; Length 177;  
Best Local Similarity 53.3%; Pred. No. 14;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15

Db 154 EKAHYEGYQVASGRA 168

RESULT 10

H86355

probable 14-3-3 protein T16I5.8 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: H86355

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: AB6141; MUID:21016719; PMID:11130712

A/Accession: H86355

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-254 <STO>

A/Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:G  
C/Genetics:

A/Map position: 1

C/Superfamily: 14-3-3 protein

Query Match 57.7%; Score 41; DB 2; Length 254;  
Best Local Similarity 90.0%; Pred. No. 20;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 EAYKAAAAAA 15

Db 151 EAYKAAVAAA 160

RESULT 11

JC4086

fatty-acid synthase (EC 2.3.1.85) alpha chain - yeast (Candida albicans)

C/Species: Candida albicans

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: JC4086

R/Southard, S.B.; Cihlar, R.L.  
Gene 156, 133-138, 1995

A/Title: Analysis and expression of the Candida albicans FAS2 gene.

A/Reference number: JC4086; MUID:95255657; PMID:7737507

A/Accession: JC4086

A/Molecule type: DNA

A/Residues: 1-1885 <SOU>

A/Cross-references: UNIPROT:P43098; GB:L29063; NID:g456442; PIDN:AAA34345.1; PID:g45644

C/Genetics:

A/Gene: fas2

A/Map position: 3

C/Superfamily: yeast fatty-acid synthase

C/Keywords: acyltransferase; coenzyme A; fatty acid biosynthesis; phosphopantetheine; p  
F;1299-1304/Region: cerulenin binding #status predicted

F;181/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 57.7%; Score 41; DB 1; Length 1885;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KAKYEAYKAA 11

Db 62 KAKYESYDAA 71

RESULT 12

T27431

hypothetical protein Y79H2A.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T27431

R/Matthews, L.  
submitted to the EMBL Data Library, September 1999

A/Reference number: Z20365

A/Accession: T27431

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2129 <WIL>

A:Cross-references: UNIPROT:Q9U1R8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:X

A:Experimental source: clone Y79H2A

C:Genetics:

A:Gene: CESP:Y79H2A.3

A:Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67

; 1760/1; 1929/3; 2037/3; 2074/3

Query Match 57.7%; Score 41; DB 2; Length 2129;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAA 12

Db 144 EYAKYERYSAA 155

#### RESULT 13

S40015

Phd protein - phage P1

C:Species: phage P1

C:Date: 25-Dec-1994 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004

C:Accession: S40015; S38553

R:Lehnher, H.; Maguin, E.; Jafri, S.; Yarmolinsky, M.B.

J. Mol. Biol. 233, 414-428, 1993

A:Title: Plasmid addition genes of bacteriophage P1: doc, which causes cell death on cu

A:Reference number: S40015; MUID:94016561; PMID:8411153

A:Accession: S40015

A:Molecule type: DNA

A:Residues: 1-73 <LEH>

A:Cross-references: UNIPROT:Q06253; GB:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

R:Schmidt, C.; Lehnher, H.; Guidolin, A.; Arber, W.

submitted to the EMBL Data Library, November 1992

A:Description: Additional late promoter sequences of bacteriophage P1.

A:Reference number: S38553

A:Accession: S38553

A:Molecule type: DNA

A:Residues: 1-73 <SCH>

A:Cross-references: EMBL:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

Query Match 56.3%; Score 40; DB 2; Length 73;

Best Local Similarity 64.3%; Pred. No. 8.8;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 KAKYEAYKAAAAA 15

Db 41 KATFEAYKKAALDA 54

#### RESULT 14

T43037

probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy

C:Species: Schizosaccharomyces pombe

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T43037

R:Yoshio, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A:Reference number: Z17323; MUID:98162722; PMID:9501991

A:Accession: T43037

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-377 <YOS>

A:Cross-references: UNIPROT:P78866; EMBL:D89216; NID:g1749639; PIDN:BAAL3877.1; PID:g174

A:Experimental source: strain PR745

C:Function:

A:Pathway: fatty acid biosynthesis

C:Superfamily: yeast fatty-acid synthase

C:Keywords: acyltransferase; coenzyme A; fatty acid biosynthesis

Query Match 56.3%; Score 40; DB 2; Length 377;

Best Local Similarity 57.1%; Pred. No. 42;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAA 14

Db 160 DEATYNAKAKTAA 173

#### RESULT 15

JV0057

tolA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C:Accession: JV0057; B64810

R:Levengood, S.K.; Webster, R.E.

J. Bacteriol. 171, 6600-6609, 1989

A:Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ

A:Reference number: JV0057; MUID:90078104; PMID:2687247

A:Accession: JV0057

A:Molecule type: DNA

A:Residues: 1-421 <LEV>

A:Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019

A:Experimental source: strain JM105

A>Note: the authors translated the initiation codon GTG for residue 1 as Val

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B64810

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-421 <BLAT>

A:Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960,

A:Experimental source: strain K-12, substrain MG1655

C:Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t

C:Genetics:

A:Gene: tolA

A:Map position: 17 min

A:Start codon: GTG

C:Keywords: nucleotide binding; P-loop; transmembrane protein

F:14-34/Domain: transmembrane #status predicted <MSS>

F:78-301/Domain: helical #status predicted <HSR>

F:355-362/Region: nucleotide-binding motif A (P-loop)

Query Match 56.3%; Score 40; DB 2; Length 421;

Best Local Similarity 76.9%; Pred. No. 47;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAA 13

Db 217 EKAKAEAEKKA 229

Search completed: February 26, 2005, 23:57:12

Job time : 17.3163 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 65.2041 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-65  
Perfect score: 71  
Sequence: 1 EKAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	63.4	300	Q9VFL4	Q9VFL4 drosophila
2	45	63.4	463	Q9V7U6	Q9V7U6 drosophila
3	45	63.4	707	Q64CP3	Q64CP3 uncultured
4	43	60.6	299	RL22_DROME	P50887 drosophila
5	43	60.6	312	Q9UAN1	Q9UAN1 drosophila
6	43	60.6	508	Q6QUT5	Q6QUT5 corynebacte
7	43	60.6	570	Q96M46	Q96M46 homo sapien
8	42	59.2	177	RL19_RHIME	Q92139 rhizobium m
9	42	59.2	179	RL19_AGR5	Q8ubz5 agrobacteri
10	42	59.2	181	RL19_RHIL0	P58168 rhizobium 1
11	42	59.2	188	HXD8_CHICK	P23459 gallus gall
12	42	59.2	289	Q81XZ1	Q81XZ1 mus musculu
13	42	59.2	289	Q81XZ1	Q81XZ1 homo sapien
14	42	59.2	290	HXD8_HUMAN	P13378 homo sapien
15	42	59.2	366	Q6FT73	Q6FT73 candida gla
16	42	59.2	395	Q6DTF3	Q6DTF3 erwinia car
17	41.5	58.5	189	Q7M495	Q7M495 homarus ame
18	41.5	58.5	189	Q7M496	Q7M496 homarus ame
19	41	57.7	165	Q64SE1	Q64SE1 bacteroides
20	41	57.7	177	MSRA_LISIN	Q92ae8 listeria in
21	41	57.7	177	MSRA_LISMO	Q8y640 listeria mo
22	41	57.7	177	Q71YF6	Q71YF6 listeria mo
23	41	57.7	254	143A_ARATH	P48347 arabidopsis
24	41	57.7	274	Q8T4I3	Q8T4I3 drosophila
25	41	57.7	274	Q9VFL3	Q9VFL3 drosophila
26	41	57.7	274	Q6UK87	Q6UK87 burkholderi
27	41	57.7	316	Q8A8P1	Q8A8P1 bacteroides
28	41	57.7	432	Q81RS8	Q81RS8 drosophila
29	41	57.7	551	CALX_PEA	O82709 pisum sativ
30	41	57.7	574	Q85XM8	Q85XM8 drosophila
31	41	57.7	607	Q9W327	Q9W327 drosophila

32	41	57.7	847	2	Q7SC23	Q7SC23 neurospora
33	41	57.7	1271	2	Q7K705	Q7K705 caenorhabdt
34	41	57.7	1878	2	Q6BWN1	Q6BWN1 debaryomyce
35	41	57.7	1885	1	FAS2_CANAL	P43098 c fatty aci
36	41	57.7	2129	2	Q9UIR8	Q9UIR8 caenorhabdt
37	40	56.3	73	1	PHD_BPPI	O06253 bacterioph
38	40	56.3	73	2	Q79A04	Q79A04 escherichia
39	40	56.3	153	2	Q7XVT5	Q7XVT5 oryza sativ
40	40	56.3	177	2	Q8LQ30	Q8LQ30 oryza sativ
41	40	56.3	281	2	Q7X2V5	Q7X2V5 uncultured
42	40	56.3	289	2	Q71WI3	Q71WI3 listeria mo
43	40	56.3	377	2	P78866	P78866 schizosacch
44	40	56.3	404	2	Q7F9Q4	Q7F9Q4 oryza sativ
45	40	56.3	413	2	Q83SA1	Q83SA1 shigella fl

ALIGNMENTS

RESULT 1  
ID Q9VFL4 PRELIMINARY; PRT; 300 AA.  
AC Q9VFL4;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE CG14840-PA (AT18408p).  
GN ORFNames=CG14840;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazef R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Muskern D.R., Pacleb J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,  
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";

```

RL Science 287:2185-2195(2000).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN (5)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN (7)
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003704; AAF55038.1; -
DR EMBL; AY089356; AAL90094.1; -
DR IntAct; Q9VFL4; -
DR FlyBase; FBgn0038217; CG14840.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;
Query Match 63.4%; Score 45; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 EKAKYEAYKAAANA 14
DB 242 EKTQAAAYKAAACAA 255
RESULT 2
ID Q9V7U6 PRELIMINARY; PRT; 463 AA.
AC Q9V7U6;

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DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE CG6301-PA.  
GN ORFNames=CG6301;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot W.L.,  
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin  
a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
RN [4]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003805; AAF57947.2; -.
DR Intact; Q9V7U6; -.
DR FlyBase; FBgn0034161; CG6301.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEFB6EBC9 CRC64;

Query Match      63.4%; Score 45; DB 2; Length 463;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKAKEYEAYKAAAAA 14
    ||| ||||| ||
DB 275 EKTQQAAYKACAA 288

RESULT 3
O64CP3 PRELIMINARY; PRT; 707 AA.
AC Q64CP3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=G21D1_21;
OS uncultured archaeon GZfos1D1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics."?
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY714833; AAU82834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match      63.4%; Score 45; DB 2; Length 707;
Best Local Similarity 73.3%; Pred. No. 66;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKAKEYEAYKAAAAA 15
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DB 645 EKLKSEAERAAAAA 659

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RESULT 4
RL22 DROME STANDARD; PRT; 299 AA.
ID RL22 DROME
AC P50887; Q9V3X9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE 60S ribosomal protein L22.
GN Name=Rpl22; ORFNames=CG7434;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Glover C.V.C., Bidwai A.P., Zhao W.F.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassatman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."?
RL Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."?
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

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RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Motlier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell I.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
CC -!- SIMILARITY: Belongs to the ribosomal protein L22e family.
CC -----
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CC -----
DR EMBL; U42587; AAB17433.1; -.
DR EMBL; AE003418; AAF45546.1; -.
DR EMBL; AL132792; CAB60023.1; -.
DR IntAct; P50887; -.
DR FlyBase; FBgn0015288; RPL22.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
DR ProDom; PD007306; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT DOMAIN 24 31 Poly-Ala.
FT DOMAIN 46 50 Poly-Ala.
FT DOMAIN 65 70 Poly-Ala.
FT DOMAIN 93 98 Poly-Ala.
FT DOMAIN 103 112 Poly-Ala.
FT DOMAIN 136 152 Poly-Ala.
FT DOMAIN 185 188 Poly-Lys.
FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).
SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;

Query Match
Best Local Similarity 60.6%; Score 43; DB 1; Length 299;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKRAAAAAA 15
Db 36 EKPKAEAAKPAAAAA 50

RESULT 5
Q9UAN1 PRELIMINARY; PRT; 312 AA.
ID Q9UAN1
AC Q9UAN1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein L22 (Fragment).
GN Name=RPL22; Synonyms=rp122;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;

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RT "poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal
RT proteins, L22 and L23a, with unique histone-like amino-terminal
RT extensions.";
RL Gene 226:339-345(1999).
DR EMBL; AF080131; AAD19341.1; -.
DR FlyBase; FBgn0015288; Rpl22.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;

Query Match
Best Local Similarity 60.6%; Score 43; DB 2; Length 312;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKYEAYKRAAAAAA 15
Db 49 EKPKAEAAKPAAAAA 63

RESULT 6
Q6QUT5 PRELIMINARY; PRT; 508 AA.
ID Q6QUT5
AC Q6QUT5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE PS2.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22243;
RX PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;
RA Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tauch A.,
RA Puhler A., Kalinowski J.;
RT "Classification of hyper-variable Corynebacterium glutamicum surface-
RT layer proteins by sequence analyses and atomic force microscopy.";
RL J. Biotechnol. 112:177-193(2004).
DR EMBL; AY525006; AAS20307.1; -.
SQ SEQUENCE 508 AA; 55416 MW; B28137E469228581 CRC64;

Query Match
Best Local Similarity 60.6%; Score 43; DB 2; Length 508;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAYKRAAAAAA 15
Db 104 EQAAYEAFAPAAAA 118

RESULT 7
Q96M46 PRELIMINARY; PRT; 570 AA.
ID Q96M46
AC Q96M46;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ32830.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;

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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Teraashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete dequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK057392; BAB71466.1; -.
DR InterPro; IPR008938; ARM.
SQ SEQUENCE 570 AA; 65769 MW; 65BEBB6F244FC7E2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 570;
Best Local Similarity 66.7%; Pred. NO. 1.2e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAA 12
DB 195 EKVKYEAYRTLA 206

RESULT 8
RL19_RHIME STANDARD; PRT; 177 AA.
AC Q92L39;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rpL5; OrderedLocustNames=R03246; ORFNames=SMC03863;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
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CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC -----
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DR EMBL; AL591793; CAC47825.1; -.
DR HAMAP; MF_00402; -.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR PRODOM; PD002979; Ribosomal_L19; 1.
DR TIGRFAMs; TIGR01024; rplS_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 177 AA; 19255 MW; 1BD19D6561AB8F22 CRC64;

Query Match 59.2%; Score 42; DB 1; Length 177;
Best Local Similarity 66.7%; Pred. NO. 56;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAA 15
DB 136 EKARIEAEKYAAAAQA 150

RESULT 9
RL19_AGR5 STANDARD; PRT; 179 AA.
AC Q8UBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rpL5; OrderedLocustNames=Atu2703, AGR_C_4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphitumachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Merkelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
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CC      aminoacyl-tRNA binding site (By similarity).
CC      -1- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AE009216; AAL43684.1; -.
DR      EMBL; AE008183; AAK88423.1; -.
DR      PIR; AF2908; AF2908.
DR      PIR; F97683; F97683.
DR      HAMAP; MF_00402; -; 1.
DR      InterPro; IPR001857; Ribosomal_L19.
DR      Pfam; PF01245; Ribosomal_L19; 1.
DR      PRINTS; PR00061; RIBOSOMALL19.
DR      ProDom; PD002979; Ribosomal_L19; 1.
DR      TIGRFAMs; TIGR01024; rplS_bact; 1.
DR      PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW      Complete proteome; Ribosomal protein.
SQ      SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

Query Match          59.2%; Score 42; DB 1; Length 179;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 EKAKEYAYKAAAAA 15
      |||: ||| ||| |
Db      137 EKARLEAEKVAQA 151

RESULT 10
RL19_RHIL0 STANDARD; PRT; 181 AA.
AC P58168;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rplS; OrderedLocustNames=ml14283;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
OK [1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RT DNA Res. 7:331-338(2000).
RL -1- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AP003003; BAB50976.1; -.

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DR      HAMAP; MF_00402; -; 1.
DR      InterPro; IPR001857; Ribosomal_L19.
DR      Pfam; PF01245; Ribosomal_L19; 1.
DR      PRINTS; PR00061; RIBOSOMALL19.
DR      ProDom; PD002979; Ribosomal_L19; 1.
DR      TIGRFAMs; TIGR01024; rplS_bact; 1.
DR      PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW      Complete proteome; Ribosomal protein.
SQ      SEQUENCE 181 AA; 19927 MW; AEF19D6593A9E835 CRC64;

Query Match          59.2%; Score 42; DB 1; Length 181;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 EKAKEYAYKAAAAA 15
      |||: ||| ||| |
Db      136 EKARIEAEKVAQA 150

RESULT 11
HXD8_CHICK STANDARD; PRT; 188 AA.
ID HXD8_CHICK
AC P23459;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Chox-M).
GN Name=HOXD8; Synonyms=CHOX-M;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
OK [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91238215; PubMed=1674560;
RX Crompton M.R., McGregor A.D., Goodwin G.H.;
RA "cDNA cloning of a homeobox-containing gene expressed in avian
RT myeloblastic virus-transformed chicken monoblastic leukaemia cells."
RL Leukemia 5:357-360(1991).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X57158; CAA40445.1; -.
DR      PIR; I50145; I50145.
DR      HSSP; P02833; 9ANT.
DR      TRANSFAC; T01754; -.
DR      InterPro; IPR001827; Antennapedia.
DR      InterPro; IPR001356; Homeobox.
DR      InterPro; IPR009057; Homeodomain like.
DR      InterPro; IPR000047; HTH_lambdarepress.
DR      Pfam; PF000046; Homeobox; 1.
DR      PRINTS; PR00025; ANTENNAPEDIA.
DR      PRINTS; PR00024; HOMEBOX.
DR      PRINTS; PR00031; HTHREPRESSR.
DR      ProDom; PD000010; Homeobox; 1.
DR      SMART; SM00389; HOX; 1.
DR      PROSITE; PS00032; ANTENNAPEDIA; 1.
DR      PROSITE; PS00027; HOMEBOX_1; 1.
DR      PROSITE; PS00071; HOMEBOX_2; 1.
KW      Developmental protein; DNA-binding; Homeobox; Nuclear protein;

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KW Transcription regulation.
FT DOMAIN 15 25 Poly-Ala.
FT SITE 83 88 Antp-type hexapeptide.
FT DNA BIND 95 154 Homeobox.
SQ SEQUENCE 188 AA; 21729 MW; D4560E8807FE29FE CRC64;

Query Match 59.2%; Score 42; DB 1; Length 188;
Best Local Similarity 81.8%; Pred. No. 59;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
   | |||||
Db 10 YSKYKAAAAA 20

RESULT 12
HXD8 MOUSE STANDARD; PRT; 289 AA.
AC P23463;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).
GN Name=Hoxd8; Synonyms=Hox-4.3, Hoxd-8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91209232; PubMed=1982431;
RA Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,
RA Falkenstein H., Duboule D.;
RT "Primary structure and embryonic expression pattern of the mouse Hox-
RT 4.3 homeobox gene.";
RL Development 110:733-745(1990).
RN [2]
RP SEQUENCE OF 191-289 FROM N.A.
RX MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;
RA Sadoul R., Featherstone M.;
RT "Sequence analysis of the homeobox-containing exon of the murine Hox-
RT 4.3 homeogene.";
RL Biochim. Biophys. Acta 1089:259-261(1991).
RN [3]
RP SEQUENCE OF 195-254 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Strock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
RN [4]
RP SEQUENCE OF 192-260 FROM N.A.
RX MEDLINE=92212934; PubMed=1348361;
RA Nazareali A., Kim Y., Nirenberg M.;
RT "Hox-1.11 and Hox-4.9 homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56561; CAA39911.1; -
DR EMBL; M87803; AAA37852.1; -

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DR PIR; A43562; A43562.
DR PIR; S16177; A41605.
DR HSSP; P02833; 9ANT.
DR TRANSPAC; T01426; -.
DR MGD; MGI:96209; Hoxd8.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 28 Poly-Ala.
FT DOMAIN 62 89 Gly/Pro-rich.
FT DOMAIN 108 117 Poly-Pro.
FT SITE 183 188 Antp-type hexapeptide.
FT DNA BIND 195 254 Homeobox.
FT CONFLICT 207 208 TL -> RV (in Ref. 1).
FT CONFLICT 231 231 T -> S (in Ref. 1).
FT CONFLICT 265 266 EA -> DG (in Ref. 1).
FT CONFLICT 275 275 A -> V (in Ref. 2).
SQ SEQUENCE 289 AA; 31410 MW; 578309F9B9B2BDFE CRC64;

Query Match 59.2%; Score 42; DB 1; Length 289;
Best Local Similarity 81.8%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
   | |||||
Db 10 YSKYKAAAAA 20

RESULT 13
Q8IXZ1 PRELIMINARY; PRT; 289 AA.
ID Q8IXZ1
AC Q8IXZ1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Homeo box D8.
GN Name=HOXD8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Straubeberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC038709; AAH38709.1; -.
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEIDIA.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; UNKNOWN_1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 289 AA; 31839 MW; 4C2621085174B447 CRC64;

Query Match
Best Local Similarity 59.2%; Score 42; DB 2; Length 289;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAA 15
   |||||
Db 10 YSKYKAAAAA 20

RESULT 14,
HXD8_HUMAN STANDARD; PRT; 290 AA.
AC P13378;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4).
GN Name=HOXD8; Synonyms=HOX4E;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Birren B., Linton L., Nusbaum C., Lander E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kosaki K., Kosaki R., Suzuki T., Yoshinashi H., Sasaki K., Matsuo N.;
RL "A complete mutation analysis panel of human HOX genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 193-287 FROM N.A.
RX MEDLINE=89306602; PubMed=2568311;
RA Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T.,
RA Sparkes R.S., de Robertis E.M.;
RT "Complementary homeo protein gradients in developing limb buds.";
RL Genes Dev. 3:641-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR EMBL; AC009336; -; NOT ANNOTATED_CDS.
DR EMBL; AY014304; AAG42152.1; -.
DR EMBL; AY014303; AAG42152.1; JOINED.
DR EMBL; X15507; CAA33529.1; -.
DR PIR; B32830; B32830.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T03332; -.
DR Genew; HGNC:5139; HOXD8.
DR MIM; 142985; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEIDIA.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DE Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 23 Poly-Ala.
FT DOMAIN 45 50 Poly-Ala.
FT DOMAIN 109 123 Poly-Pro.
FT DNA_BIND 197 256 Homeobox.
FT CONFLICT 287 287 G -> A (in Ref. 3).
SQ SEQUENCE 290 AA; 31910 MW; 75FF95A73E2A85F CRC64;

Query Match
Best Local Similarity 59.2%; Score 42; DB 1; Length 290;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 YEAYKAAAAA 15
   |||||
Db 10 YSKYKAAAAA 20

RESULT 15
O6FT73 PRELIMINARY; PRT; 366 AA.
ID O6FT73;
AC O6FT73;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Similar to sp|P40319 Saccharomyces cerevisiae YLR372w SUR4 sterol
DE isomerase.
GN ORFNames=CAGL0G04851g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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RA Hanttraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Boloitin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.,  
RT "Genome evolution in yeasts."  
RL Nature 430:35-44(2004).  
DR EMBL; CR380953; CAG59498.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
DR InterPro; IPR002076; GNS1\_SUR4.  
DR Pfam; PF01151; ELO; 1.  
DR PROSITE; PS01188; ELO; 1.  
KW Isomerase.  
SQ SEQUENCE 366 AA; 41202 MW; 29E7E159FF08BB76 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 366;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15  
:||:|||||:  
Db 335 KKAKEKEAKAAAAA 349

Search completed: February 26, 2005, 23:55:37  
Job time : 70.2041 secs

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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 97.1327 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-89  
Perfect score: 93  
Sequence: 1 APEKAKYEAYKAAAAAPA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	19	5	ABP52295 HLA-DR2 m
2	82	88.2	17	5	ABP52294 HLA-DR2 m
3	82	88.2	17	5	ABP52296 HLA-DR2 m
4	73	78.5	17	5	ABP52303 HLA-DR2 m
5	71	76.3	15	5	ABP52271 HLA-DR2 m
6	71	76.3	15	5	ABP52298 HLA-DR2 m
7	69	74.2	17	5	ABP52302 HLA-DR2 m
8	65	69.9	15	5	ABP52270 HLA-DR2 m
9	63	67.7	15	5	ABP52301 HLA-DR2 m
10	61	65.6	15	5	ABP52291 HLA-DR2 m
11	61	65.6	15	5	ABP52263 HLA-DR2 m
12	60	64.5	15	5	ABP52272 HLA-DR2 m
13	59	63.4	15	5	ABP52259 HLA-DR2 m
14	59	63.4	15	5	ABP52257 HLA-DR2 m
15	57	61.3	15	5	ABP52297 HLA-DR2 m
16	56	60.2	15	5	ABP52253 HLA-DR2 m
17	56	60.2	15	5	ABP52251 HLA-DR2 m
18	56	60.2	15	5	ABP52239 HLA-DR2 m
19	55	59.1	15	5	ABP52290 HLA-DR2 m
20	55	59.1	15	5	ABP52261 HLA-DR2 m
21	55	59.1	15	5	ABP52244 HLA-DR2 m
22	55	59.1	15	5	ABP52292 HLA-DR2 m
23	55	59.1	15	5	ABP52269 HLA-DR2 m
24	55	59.1	15	5	ABP52262 HLA-DR2 m
25	54	58.1	15	5	ABP52264 HLA-DR2 m

26	54	58.1	15	5	ABP52267 HLA-DR2 m
27	54	58.1	15	5	ABP52236 HLA-DR2 m
28	54	58.1	442	4	ABP62945 Drosophila
29	53	57.0	15	5	ABP52299 HLA-DR2 m
30	52	55.9	15	5	ABP52265 HLA-DR2 m
31	51	54.8	15	5	ABP52254 HLA-DR2 m
32	51	54.8	15	5	ABP52255 HLA-DR2 m
33	51	54.8	15	5	ABP52240 HLA-DR2 m
34	51	54.8	15	5	ABP52241 HLA-DR2 m
35	51	54.8	15	5	ABP52304 HLA-DR2 m
36	51	54.8	15	5	ABP52248 HLA-DR2 m
37	51	54.8	15	5	ABP52249 HLA-DR2 m
38	50	53.8	15	5	ABP52232 HLA-DR2 m
39	50	53.8	15	5	ABP52268 HLA-DR2 m
40	50	53.8	15	5	ABP52231 HLA-DR2 m
41	50	53.8	570	6	ADA5549 Human pro
42	50	53.8	570	7	ADJ70708 Human hea
43	49	52.7	15	5	ABP52235 HLA-DR2 m
44	49	52.7	15	5	ABP52250 HLA-DR2 m
45	48	51.6	15	3	Aay58982 Copeptide

ALIGNMENTS

RESULT 1	ABP52295	ABP52295 standard; peptide; 19 AA.
ID	ABP52295	16-OCT-2002 (first entry)
XX	AC	ABP52295;
XX	DT	HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX	DE	Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
XX	KW	anti-tumour necrosis factor agent.
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	PN	WO200259143-A2.
XX	PD	01-AUG-2002.
XX	PF	24-JAN-2002; 2002WO-US002071.
XX	PR	24-JAN-2001; 2001US-0263569P.
PA	XX	(HARD ) HARVARD COLLEGE.
PI	XX	Strominger JL, Fridkis-Hareli M;
XX	DR	WPI; 2002-608439/65.
XX	PT	New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
XX	PT	Claim 28; Page 39; 54pp; English.
XX	PS	The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases
CC	CC	

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 19 AA;  
  
Query Match 100.0%; Score 93; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 APEKAKYEAYKAAAAAPA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 APEKAKYEAYKAAAAAPA 19  
  
RESULT 2  
ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 17 AA;  
  
Query Match 88.2%; Score 82; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 APEKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 APEKAKYEAYKAAAAA 17  
  
RESULT 3  
ABP52296 standard; peptide; 17 AA.  
XX  
AC ABP52296;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
  
Query Match 88.2%; Score 82; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 EKAKYEAYKAAAAAPA 19

DB 1 EKAKEYAYKAAAAA 17

RESULT 4  
ID ABP52303 standard; peptide; 17 AA.  
XX AC ABP52303;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
XX KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KM immune response; antiinflammatory; neuroprotective; proliferation;  
KM MHC class II protein inhibitor; demyelinating disease; inhibition;  
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KM anti-tumour necrosis factor agent.  
XX OS Homo sapiens.  
OS Synthetic.  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX SQ Sequence 17 AA;

Query Match 78.5%; Score 73; DB 5; Length 17;  
Best Local Similarity 88.2%; Pred. No. 0.00022;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17  
DB 1 APEKAKFEAYKAAAAA 17

RESULT 5  
ID ABP52271 standard; peptide; 15 AA.

XX AC ABP52271;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
XX KM Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KM HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KM immune response; antiinflammatory; neuroprotective; proliferation;  
KM MHC class II protein inhibitor; demyelinating disease; inhibition;  
KM post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KM anti-tumour necrosis factor agent.  
XX OS Homo sapiens.  
OS Synthetic.  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX SQ Sequence 15 AA;

Query Match 76.3%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKAKEYAYKAAAAA 17  
DB 1 EKAKEYAYKAAAAA 15

RESULT 6  
ID ABP52298 standard; peptide; 15 AA.  
XX AC ABP52298;  
XX DT 16-OCT-2002 (first entry)  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:92.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX PS  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
XX SQ Sequence 15; AA;  
XX  
Query Match 76.3%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | | | | |  
Db 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | | |  
RESULT 7  
ABP52302 standard; peptide; 17 AA.  
XX ID  
XX AC ABP52302;  
XX  
XX DT 16-OCT-2002 (first entry)  
XX  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
XX  
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX PS  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
XX SQ Sequence 17 AA;  
XX  
Query Match 74.2%; Score 69; DB 5; Length 17;  
Best Local Similarity 82.4%; Pred. No. 0.00092;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 APEKAYEAYKAAAAA 17  
| | | | | : | | | | | | | | | | | |  
Db 1 APEKAYEAYKAAAAA 17  
| | | | | : | | | | | | | | | | | |  
RESULT 8  
ABP52270 standard; peptide; 15 AA.  
XX ID  
XX AC ABP52270;  
XX  
XX DT 16-OCT-2002 (first entry)  
XX  
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:64.  
XX  
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200259143-A2.  
XX PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 69.9%; Score 65; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.0034;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 EKAKYEAYKAAAAA 17  
XX |:::|:::|:::|:::|:::|  
XX 1 EAKYEAYKAAAAA 15  
Db  
RESULT 9  
ABP52301 standard; peptide; 15 AA.  
XX  
XX ABP52301;  
AC  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:95.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI

XX  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
XX  
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CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 67.7%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0069;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EKAKYEAYKAAAAA 17  
XX |:::|:::|:::|:::|:::|  
XX 1 EAKFEAYKAAAAA 15  
Db  
RESULT 10  
ABP52291  
ID ABP52291 standard; peptide; 15 AA.  
XX  
XX ABP52291;  
AC  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:85.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO200259143-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
PI

XX Claim 28; Page 39; 54pp; English.  
PS  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
SQ Sequence 15 AA;  
  
Query Match 65.6%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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|:|||||  
Db 1 EKPKYEAYKAAAAA 15  
  
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ID ABP52263 standard; peptide; 15 AA.  
XX  
AC ABP52263;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:57.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Example 1; Page 33; 54pp; English.  
PS  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
CC  
XX  
SQ Sequence 15 AA;  
  
Query Match 65.6%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.014;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
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|:|||||  
Db 1 EKAKYEAYKAAAAA 15  
  
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XX  
AC ABP52272;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:66.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
PS  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 15 AA;

Query Match 64.5%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEYAYKAAAAA 17  
| | | | | | | | | |  
DB 1 EAKYAYKAAAAA 15

RESULT 13  
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ID ABP52259 standard; peptide; 15 AA.  
XX  
AC ABP52259;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:53.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 33; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;

Query Match 63.4%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.029;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEYAYKAAAAA 17  
| | | | | | | | | |  
DB 1 EKAAYAYKAAAAA 15

RESULT 14  
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ID ABP52257 standard; peptide; 15 AA.  
XX  
AC ABP52257;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 32; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;

Query Match 63.4%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.029;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
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KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKPKFEAYKAAAAA 15
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Search completed: February 26, 2005, 23:48:22  
Job time : 97.1327 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 25.398 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-89  
Perfect score: 93  
Sequence: 1 APEKAKYEAYKAAAAAPA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	51.6	118	US-09-101-751A-46	Sequence 46, Appl
2	47.5	51.1	219	US-09-902-540-16623	Sequence 16623, A
3	47	50.5	612	US-09-252-991A-25727	Sequence 25727, A
4	45	48.4	137	US-10-081-817A-30	Sequence 30, Appl
5	45	48.4	595	US-10-052-092-31	Sequence 31, Appl
6	45	48.4	1001	US-09-248-796A-18658	Sequence 18658, A
7	44.5	47.8	324	US-09-248-796A-17156	Sequence 17156, A
8	44.5	47.8	596	US-08-836-620A-16	Sequence 16, Appl
9	44	47.3	405	US-09-328-352-4239	Sequence 4239, Ap
10	43	46.2	55	US-09-902-540-9849	Sequence 9849, Ap
11	43	46.2	162	US-09-732-210-1445	Sequence 1445, Ap
12	43	46.2	172	US-09-902-540-13256	Sequence 13256, A
13	43	46.2	419	US-09-489-039A-13260	Sequence 13260, A
14	42	45.2	13	PCT-US95-04121-38	Sequence 38, Appl
15	42	45.2	38	US-09-117-121-16	Sequence 16, Appl
16	42	45.2	38	US-09-117-121-24	Sequence 16, Appl
17	42	45.2	38	US-09-344-529-5	Sequence 5, Appl
18	42	45.2	136	US-09-732-210-630	Sequence 630, App
19	42	45.2	136	US-09-711-164-303	Sequence 303, App
20	42	45.2	136	US-09-492-709A-385	Sequence 385, App
21	42	45.2	178	US-09-252-991A-20280	Sequence 20280, A
22	42	45.2	189	US-09-902-540-12588	Sequence 12588, A
23	42	45.2	190	US-09-902-540-14713	Sequence 14713, A
24	42	45.2	220	US-09-902-540-9904	Sequence 9904, Ap
25	42	45.2	273	US-09-910-430-34	Sequence 34, Appl
26	42	45.2	318	US-09-270-767-45996	Sequence 45996, A
27	42	45.2	519	US-09-902-540-15378	Sequence 15378, A

28	42	45.2	538	4	US-09-616-289-43	Sequence 43, Appl
29	41.5	44.6	1156	4	US-09-902-540-15564	Sequence 15564, A
30	41	44.1	54	3	US-09-117-121-30	Sequence 30, Appl
31	41	44.1	56	4	US-09-405-743A-3	Sequence 3, Appl
32	41	44.1	56	4	US-09-816-989A-3	Sequence 3, Appl
33	41	44.1	77	4	US-09-405-743A-5	Sequence 5, Appl
34	41	44.1	77	4	US-09-816-989A-5	Sequence 5, Appl
35	41	44.1	86	4	US-09-405-743A-6	Sequence 6, Appl
36	41	44.1	86	4	US-09-816-989A-6	Sequence 6, Appl
37	41	44.1	102	4	US-09-101-751A-90	Sequence 90, Appl
38	41	44.1	166	4	US-09-252-991A-22139	Sequence 22139, A
39	41	44.1	218	4	US-09-101-751A-48	Sequence 48, Appl
40	41	44.1	245	4	US-09-902-540-12314	Sequence 12314, A
41	41	44.1	287	3	US-09-105-697-7	Sequence 7, Appl
42	41	44.1	287	3	US-09-105-697-8	Sequence 8, Appl
43	41	44.1	288	3	US-09-105-697-3	Sequence 3, Appl
44	41	44.1	291	3	US-09-105-697-4	Sequence 4, Appl
45	41	44.1	291	3	US-09-105-697-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 46, Application US/09101751A  
; Patent No. 6465253  
; GENERAL INFORMATION:  
; APPLICANT: WICKHAM, THOMAS J.  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BROUGH, DOUGLAS E.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS  
; FILE REFERENCE: 85710  
; CURRENT APPLICATION NUMBER: US/09/101,751A  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: WO 96US19150  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 08/700,846  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/701,124  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/563,368  
; PRIOR FILING DATE: 1995-11-28  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1..7)  
; OTHER INFORMATION: Description of Unknown Organism: Artificial  
; US-09-101-751A-46

Query Match 51.6%; Score 48; DB 4; Length 118;  
Best Local Similarity 61.1%; Pred. No. 2;  
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAAAPA 19  
DB 68 PEKRAEAFAAAAEAAAPA 85

RESULT 2  
US-09-902-540-16623  
; Sequence 16623, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.

```

; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR APPLICATION NUMBER: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16623
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16623

Query Match
Best Local Similarity 51.1%; Score 47.5; DB 4; Length 219;
Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAYEAYKAAAAAPA 19
Db 189 AEEKARAET-EAAAAAPA 206

RESULT 3
US-09-252-991A-25727
; Sequence 25727; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25727
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25727

Query Match
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Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAYEAYKAAAAAPA 19
Db 206 PDPAQYRAWRGARSAPA 223

RESULT 4
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; Sequence 30; Application US/10081817A
; Patent No. 6815166
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Porter, Dale
; APPLICANT: Sgroi, Dennis
; APPLICANT: Krop, Ian
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 00530-094001
; CURRENT APPLICATION NUMBER: US/10/081,817A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/270,973
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 30
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-081-817A-30

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Best Local Similarity 48.4%; Score 45; DB 4; Length 137;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAAPA 19
Db 75 APVAAAYTAPVAAAYAPA 93

RESULT 5
US-10-052-092-31
; Sequence 31; Application US/10052092
; Patent No. 6821732
; GENERAL INFORMATION:
; APPLICANT: Fugua, Suzanne
; APPLICANT: Allred, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeuti
; FILE REFERENCE: P02102US2
; CURRENT APPLICATION NUMBER: US/10/052,092
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,990
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/304,018
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
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; ORGANISM: Pig
US-10-052-092-31

Query Match
Best Local Similarity 48.4%; Score 45; DB 4; Length 595;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAYEAYKAAAAAP 18
Db 55 PEGAAVDFNAAAAASAP 71

RESULT 6
US-09-248-796A-18658
; Sequence 18658; Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18658
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkn
```

US-09-248-796A-18658

Query Match 48.4%; Score 45; DB 4; Length 1001;  
Best Local Similarity 75.0%; Pred. No. 64;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 KAKYKAYKAAAAAPA 19  
||| ||| ||| ||| ||| |||  
DB 818 KAKEEAEAAAAAAA 833

RESULT 7

US-09-248-796A-17156  
; Sequence 17156, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248, 796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074, 725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096, 409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17196  
; LENGTH: 324  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-17156

Query Match 47.8%; Score 44.5; DB 4; Length 324;  
Best Local Similarity 66.7%; Pred. No. 22;  
Matches 12; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 APEKAYEYKAAAAAPA 18  
||| ||| ||| ||| ||| |||  
DB 157 APEKAKE--SAPAAAP 171

RESULT 8

US-08-836-620A-16  
; Sequence 16, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836, 620A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP96/03933  
; FILING DATE:  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 596 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; ORIGINAL SOURCE:

; ORGANISM: Rattus rattus

US-08-836-620A-16

Query Match 47.8%; Score 44.5; DB 2; Length 596;  
Best Local Similarity 66.7%; Pred. No. 44;  
Matches 12; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 PEKAYEYKAAAAAPA 19  
||| ||| ||| ||| ||| |||  
DB 55 PEGAYE-FNAAAAAAA 71

RESULT 9

US-09-328-352-4239  
; Sequence 4239, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328, 352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4239  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4239

Query Match 47.3%; Score 44; DB 4; Length 405;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 AKYKAYKAAAAAPA 19  
||| ||| ||| ||| ||| |||  
DB 81 AQFEAGAGAAAAAPA 95

RESULT 10

US-09-902-540-9849  
; Sequence 9849, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902, 540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217, 883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 9849  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-9849

Query Match 46.2%; Score 43; DB 4; Length 55;  
Best Local Similarity 52.9%; Pred. No. 5.4;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 EKAYEYKAAAAAPA 19  
||| ||| ||| ||| ||| |||  
DB 2 ETAREQAYAEASACPA 18

```

RESULT 11
US-09-732-210-1445
; Sequence 1445, Application US/09733210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Miltanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1445
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-732-210-1445

```

Query Match	46.2%;	Score 43;	DB 4;	Length 162;
Best Local Similarity	52.9%;	Pred. NO. 18;		
Matches	9;	Conservative	3;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
QY      1 APEKAKYEAYKAAAAAA 17
          ||: || | : || |||
Db      97 APKPSKLEVFNAALAA 113
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```

RESULT 12
US-09-902-540-13256
; Sequence 13256, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883.
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13256
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13256

```

Query Match	46.28;	Score 43;	DB 4;	Length 172;
Best Local Similarity	83.38;	Pred. NO. 19;		
Matches 10;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY 8 EAYKAAAAAPA 19  
||| ||| ||| |||  
Db 160 EAQKAAKAAAPA 171

```

RESULT 13
US-09-489-039A-13260
; Sequence 13260, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

```

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13260
;
; LENGTH: 419
;
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13260

Query Match          46.2%; Score 43; DB 4; Length 419;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```
QY      1 APEKAKYEAYKAAAAAPA 19
        || : : || || || ||
Db     164 AAPAPAEAKAPAAAPAAAPA 182
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```

1      RESULT 14
2      PCT-US95-04121-38
3      ; Sequence 38. Application PC/TUS9504121
4      ; GENERAL INFORMATION:
5      ;   APPLICANT:
6      ;   TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
7      ;   NUMBER OF SEQUENCES: 62
8      ;   COMPUTER READABLE FORM:
9      ;       MEDIUM TYPE: Floppy disk
10     ;   COMPUTER: IBM PC compatible
11     ;   OPERATING SYSTEM: PC-DOS/MS-DOS
12     ;   SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
13     ;   CURRENT APPLICATION DATA:
14     ;       APPLICATION NUMBER: PCT/US95/04121
15     ;   FILING DATE:
16     ;       CLASSIFICATION:
17     ;       PRIOR APPLICATION DATA:
18     ;           APPLICATION NUMBER: 08/222,206
19     ;           FILING DATE: April 1, 1994
20     ;   ATTORNEY/AGENT INFORMATION:
21     ;       NAME: Vanstone, Darlene A.
22     ;       REGISTRATION NUMBER: 35,279
23     ;       REFERENCE/DOCKET NUMBER: 079.2PCT
24     ;   TELECOMMUNICATION INFORMATION:
25     ;       TELEPHONE: (617) 466-6000
26     ;       TELEFAX: (617) 466-6010
27     ;   INFORMATION FOR SEQ ID NO: 38:
28     ;       SEQUENCE CHARACTERISTICS:
29     ;           LENGTH: 13 amino acids
30     ;           TYPE: amino acid
31     ;       STRANDEDNESS:
32     ;           TOPOLOGY: linear
33     ;       MOLECULE TYPE: peptide
34     ;       FRAGMENT TYPE: internal
35     ;
36     PCT-US95-04121-38

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Query Match	45.2%	Score 42;	DB 5;	Length 13;
Best Local Similarity	76.9%	Pred. No. 1.6;		
Matches 10;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	5	AKYEAYKAAAAA	17
		:	
Db	1	AAAYKAAKAAAAAA	13

RESULT 15  
US-09-117-121-16  
; Sequence 16, Application US/09117121  
; Patent No. 6307020  
; GENERAL INFORMATION:

```

1  APPLICANT: Hew, Choy
2  APPLICANT: Gong, Zhiyuan
3  TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
4  TITLE OF INVENTION: and Nucleic Acids
5  NUMBER OF SEQUENCES: 46
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Townsend and Townsend and Crew LLP
8  STREET: Two Embarcadero Center, Eighth Floor
9  CITY: San Francisco
10 STATE: California
11 COUNTRY: USA
12 ZIP: 94111-3834
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent in Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/117,121
20 FILING DATE: 20-NOV-1998
21 CLASSIFICATION: 435
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: WO PCT/CA97/00062
24 FILING DATE: 30-JAN-1997
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Weber, Kenneth A.
27 REGISTRATION NUMBER: 31,677
28 REFERENCE/DOCKET NUMBER: 016252-001610US
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (415) 576-0200
31 TELEFAX: (415) 576-0300
32 INFORMATION FOR SEQ ID NO: 16:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 38 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38 US-09-117-121-16

```

Query Match	45.2%	Score 42;	DB 3;	Length 38;
Best Local Similarity	63.2%;	Pred. No. 5.2;		
Matches 12;	Conservative	0;	Mismatches 7;	Indels 0;
0y	1 APEKAKYEAYKAAAAAPA	19		
Db	13 AAAKAAAEATKAAAKAAA	31		

Search completed: February 26, 2005, 23:59:29  
Job time : 26.398 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 67.8571 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-89  
Perfect score: 93  
Sequence: 1 APEKAKYEAYKAAAAAPA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	19	US-10-056-583-89	Sequence 89, Appl
2	82	88.2	17	US-10-056-583-88	Sequence 88, Appl
3	82	88.2	17	US-10-056-583-90	Sequence 90, Appl
4	73	78.5	17	US-10-056-583-97	Sequence 97, Appl
5	71	76.3	15	US-10-056-583-65	Sequence 65, Appl
6	69	74.2	17	US-10-056-583-96	Sequence 96, Appl
7	65	69.9	15	US-10-056-583-64	Sequence 64, Appl
8	63	67.7	15	US-10-056-583-95	Sequence 95, Appl
9	62	66.7	15	US-10-056-583-92	Sequence 92, Appl
10	61	65.6	15	US-10-056-583-57	Sequence 57, Appl
11	61	65.6	15	US-10-056-583-85	Sequence 85, Appl
12	60	64.5	15	US-10-056-583-66	Sequence 66, Appl
13	59	63.4	15	US-10-056-583-51	Sequence 51, Appl

14	59	63.4	15	14	US-10-056-583-53	Sequence 53, Appl
15	57	61.3	15	14	US-10-056-583-91	Sequence 91, Appl
16	56	60.2	15	14	US-10-056-583-33	Sequence 33, Appl
17	56	60.2	15	14	US-10-056-583-45	Sequence 45, Appl
18	56	60.2	15	14	US-10-056-583-47	Sequence 47, Appl
19	55	59.1	15	14	US-10-056-583-38	Sequence 38, Appl
20	55	59.1	15	14	US-10-056-583-55	Sequence 55, Appl
21	55	59.1	15	14	US-10-056-583-56	Sequence 56, Appl
22	55	59.1	15	14	US-10-056-583-63	Sequence 63, Appl
23	55	59.1	15	14	US-10-056-583-84	Sequence 84, Appl
24	55	59.1	15	14	US-10-056-583-86	Sequence 86, Appl
25	54	58.1	15	14	US-10-056-583-30	Sequence 30, Appl
26	54	58.1	15	14	US-10-056-583-58	Sequence 58, Appl
27	54	58.1	15	14	US-10-056-583-61	Sequence 61, Appl
28	53	57.0	15	14	US-10-056-583-93	Sequence 93, Appl
29	52	55.9	15	14	US-10-056-583-59	Sequence 59, Appl
30	51	54.8	15	14	US-10-056-583-34	Sequence 34, Appl
31	51	54.8	15	14	US-10-056-583-35	Sequence 35, Appl
32	51	54.8	15	14	US-10-056-583-42	Sequence 42, Appl
33	51	54.8	15	14	US-10-056-583-43	Sequence 43, Appl
34	51	54.8	15	14	US-10-056-583-48	Sequence 48, Appl
35	51	54.8	15	14	US-10-056-583-49	Sequence 49, Appl
36	51	54.8	15	14	US-10-056-583-98	Sequence 98, Appl
37	50	53.8	15	14	US-10-056-583-25	Sequence 25, Appl
38	50	53.8	15	14	US-10-056-583-26	Sequence 26, Appl
39	50	53.8	15	14	US-10-056-583-62	Sequence 62, Appl
40	50	53.8	15	15	US-10-094-749-3117	Sequence 3117, Ap
41	50	53.8	16	16	US-10-408-765A-2514	Sequence 2514, Ap
42	49	52.7	15	14	US-10-056-583-29	Sequence 29, Appl
43	49	52.7	15	14	US-10-056-583-44	Sequence 44, Appl
44	48	51.6	15	9	US-09-765-301-19	Sequence 19, Appl
45	48	51.6	15	10	US-09-765-644A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-056-583-89

Sequence 89, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 89

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-89

Query Match 100.0%; Score 93; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAAPA 19  
|||||  
Db 1 APEKAKYEAYKAAAAAPA 19

RESULT 2  
US-10-056-583-88

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; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
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Query Match      88.2%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 APEKAKYEAYKAAAAA 17
        |||||:|||||
Db      1 APEKAKYEAYKAAAAA 17
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RESULT 3
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
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Query Match      88.2%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      3 EKAKYEAYKAAAAAPA 19
        |||||:|||||
Db      1 EKAKYEAYKAAAAAPA 17
```

```
RESULT 4
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match      78.5%; Score 73; DB 14; Length 17;
Best Local Similarity 88.2%; Pred. No. 0.00016;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 APEKAKYEAYKAAAAA 17
        |||||:|||||
Db      1 APEKAKYEAYKAAAAA 17
```

```
RESULT 5
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match      76.3%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 EKAKYEAYKAAAAA 17
        |||||:|||||
Db      1 EKAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match          74.2%; Score 69; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00065;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 APEKAYEAYKAAAAA 17
Db      1 APEKAYEAYKAAAAA 17

RESULT 7
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

Query Match          69.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0024;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      3 EKAKEYEAYKAAAAA 17
Db      1 EKAKEYEAYKAAAAA 15

RESULT 8
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match          67.7%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0048;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      3 EKAKEYEAYKAAAAA 17
Db      1 EKAKEYEAYKAAAAA 15

RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match          66.7%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0069;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      3 EKAKEYEAYKAAAAA 17
Db      1 EKAKEYEAYKAAAAA 15

RESULT 10
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-57

Query Match 65.6%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0098;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAA 17  
|:|||||  
Db 1 EAKYAAAYKAAAAA 15

RESULT 11  
US-10-056-583-85

Sequence 85, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 85  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-85

Query Match 65.6%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0098;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAA 17  
|:|||||  
Db 1 EKPXEAYKAAAAA 15

RESULT 12  
US-10-056-583-66

Sequence 66, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 66  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 64.5%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.014;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAA 17  
|:|||||  
Db 1 EAKYEAAYKAAAAA 15

RESULT 13  
US-10-056-583-51

Sequence 51, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 63.4%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAA 17  
|:|||||  
Db 1 EAKYAAAYKAAAAA 15

RESULT 14  
US-10-056-583-53

Sequence 53, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
TITLE OF INVENTION: CONDITIONS  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 53  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-53

Query Match 63.4%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAA 17  
|:|||||  
Db 1 EKAAYAAAYKAAAAA 15

RESULT 15

US-10-056-583-91  
; Sequence 91, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-91

Query Match 61.3%; Score 57; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.041;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKAKYEAYKAAAAA 17  
|||:|||||||  
Db 1 EKPKFEAYKAAAAA 15

Search completed: February 27, 2005, 00:05:23  
Job time : 68.8571 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 16.8673 Seconds  
(without alignments)  
108.382 Million cell updates/sec

Title: US-10-056-583A-89  
Perfect score: 93  
Sequence: 1 APEKAKYEAYKAAAAAPPA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	58.1	441	2 A43555	GAP-43-related protein
2	49	52.7	641	2 PH1919	FL-160-4 protein -
3	48	51.6	129	1 TNLJG2	trans-activating t
4	47	50.5	106	1 TNLJG2	trans-activating t
5	47	50.5	108	2 F97521	VCO33 protein homo
6	47	50.5	108	2 AH2740	conserved hypotet
7	47	50.5	599	1 QRMSE	estrogen receptor
8	46	49.5	179	2 F97683	50S ribosomal prot
9	46	49.5	339	2 AF2908	chitinase (EC 3.2.
10	46	49.5	339	2 S39979	chitinase (EC 3.2.
11	46	49.5	340	2 S40414	chitinase (EC 3.2.
12	45	48.4	84	2 T23177	hypothetical prote
13	45	48.4	107	2 AB3271	hypothetical prote
14	45	48.4	154	2 H61076	conserved hypotet
15	45	48.4	154	2 B81866	conserved hypotet
16	45	48.4	188	2 150145	homeotic protein H
17	45	48.4	289	2 A43562	homeotic protein H
18	45	48.4	329	2 D96030	hypothetical prote
19	45	48.4	347	2 A81794	probable rotamase
20	45	48.4	348	2 B81216	peptidyl-prolyl ci
21	45	48.4	447	2 AB3359	dihydrolipamide S
22	45	48.4	595	2 147140	estradiol receptor
23	44.5	47.8	189	2 S77930	exoskeletal protei
24	44.5	47.8	189	2 S77935	exoskeletal protei
25	44.5	47.8	600	1 QRRTE	estrogen receptor
26	44	47.3	168	2 T34804	hypothetical prote
27	44	47.3	270	2 T31225	traf protein homol
28	44	47.3	282	2 T51013	related to calmodu
29	44	47.3	398	2 T21061	hypothetical prote

30	44	47.3	421	2 JV0057	tolA protein - Bsc
31	44	47.3	503	1 VMUT1B	variant surface gl
32	44	47.3	751	2 D72338	(p) pGpp synthetas
33	43.5	46.8	192	1 MOCH1A	myosin alkali 11gh
34	43	46.2	49	2 PX0029	protein C inhibito
35	43	46.2	136	2 A10026	50S ribosomal prot
36	43	46.2	162	2 H70927	probable rpsp prot
37	43	46.2	176	2 G87606	transcription regu
38	43	46.2	185	2 S36290	T-cell receptor ga
39	43	46.2	379	2 T08277	carotenoid biosynt
40	43	46.2	436	2 I51237	translation elonga
41	43	46.2	436	2 S20060	translation elonga
42	43	46.2	736	2 D96830	probable heat-shoc
43	42	45.2	109	2 T02039	acidic ribosomal p
44	42	45.2	109	2 T02716	acidic ribosomal p
45	42	45.2	136	1 R5EC16	ribosomal protein

ALIGNMENTS

RESULT 1  
A43555  
GAP-43-related protein - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C/Accession: A43555; S65398  
R/NG, S.C.; Perkins, L.A.; Conboy, G.; Perrimon, N.; Fishman, M.C.  
Development 105, 629-638, 1989  
A/Title: A Drosophila gene expressed in the embryonic CNS shares one conserved domain w  
A/Reference number: A43555; MUID:90126372; PMID:2693037  
A/Accession: A43555  
A/Molecule type: mRNA  
A/Residues: 1-441 <NGA>  
A/Cross-references: UNIPROT:P29746; EMBL:X63828  
R/Perkins, L.A.  
submitted to the EMBL Data Library, December 1991  
A/Reference number: S65398  
A/Accession: S65398  
A/Molecule type: mRNA  
A/Residues: 1-111, 'AIPKKT', 120, 'BEAK', 125, 'AOENA', 131, 'VEAEKKQEKTA', 146, 'EPTVEAQ',  
A/Cross-references: EMBL:X63828; NID:97663; PID:97664  
A/Note: the differences in residues 112-178 are due to frameshift errors  
C/Genetics:  
A/Gene: FlyBase:bhb  
A/Cross-references: FlyBase:FBgn0001090  
A/Map position: 10  
Query Match 58.1%; Score 54; DB 2; Length 441;  
Best Local Similarity 63.2%; Pred. No. 1.6;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 APEKAKYEAYKAAAAAPPA 19  
DB 263 APEKKSIESSPAAAAAPPA 281  
RESULT 2  
PH1919  
FL-160-4 protein - Trypanosoma cruzi (fragment)  
C/Species: Trypanosoma cruzi  
C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
C/Accession: PH1919; S32017  
R/Van Voorthuis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.  
J. Exp. Med. 178, 681-694, 1993  
A/Title: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene family and  
A/Reference number: JH0823; MUID:93340646; PMID:7688032  
A/Accession: PH1919  
A/Molecule type: DNA  
A/Residues: 1-641 <VAN>  
A/Cross-references: UNIPROT:Q05508  
R/van Voorthuis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.  
submitted to the EMBL Data Library, February 1993

A:Description: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene family  
A:Reference number: S32015  
A:Accession: S32017  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-289, 'L', 291-309, 'N', 311-641 <VA2>  
A:Cross-references: EMBL:X70950; NID:g11162; PID:g11163  
C:Keywords: glycoprotein  
F:115,130,224,575,590/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
Best Local Similarity 52.7%; Score 49; DB 2; Length 641;  
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAAAAPA 19  
Db 376 SPEKSKNEXSAGSGQAPS 394

## RESULT 3

trans-activating transcription regulator - simian immunodeficiency virus (macaque isolat  
C:Species: simian immunodeficiency virus, SIV  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: F28887  
R:Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.  
Nature 328, 543-547, 1987  
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to  
A:Reference number: A28887; MUID:87287230; PMID:3649576  
A:Accession: F28887  
A:Molecule type: DNA  
A:Residues: 1-129 <CHA>  
A:Cross-references: UNIPROT:P05911; GB:Y00277; GB:M16403; NID:g61730  
C:Genetics:  
A:Gene: tat  
A:Introns: 98/3  
C:Superfamily: AIDS trans-activating transcription regulator  
C:Keywords: AIDS; immunodeficiency; transcription

Query Match  
Best Local Similarity 51.6%; Score 48; DB 1; Length 129;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PEKAKYEAYKAAAAAPA 18  
Db 109 PKKAKKETVEAAVATAP 125

## RESULT 4

trans-activating transcription regulator - simian immunodeficiency virus SIVagm (type 3,  
C:Species: simian immunodeficiency virus SIVagm  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: A26737  
R:Hirsch, V.; Riedel, N.; Mullins, J.I.  
Cell 49, 307-319, 1987  
A:Title: The genome organization of STLV-3 is similar to that of the AIDS virus except f  
A:Reference number: A26737; MUID:87187627; PMID:3646094  
A:Accession: A26737  
A:Molecule type: DNA  
A:Residues: 1-106 <HIR>  
A:Cross-references: UNIPROT:P11263; GB:M19499; NID:g334657  
A:Note: the authors translated the codon GAC for residue 9 as Asn  
C:Genetics:  
A:Gene: tat  
A:Introns: 74/2  
C:Superfamily: AIDS trans-activating transcription regulator  
C:Keywords: AIDS; transcription

Query Match  
Best Local Similarity 50.5%; Score 47; DB 1; Length 106;  
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PEKAKYEAYKAAAAAPA 18  
Db 86 PEKAKKETVEAAVATAP 102

## RESULT 5

F97521  
VCO3 protein homolog (AF179595) [imported] - Agrobacterium tumefaciens (strain C58, Ce  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: F97521  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.,  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: F97521  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <KUR>  
A:Cross-references: UNIPROT:Q8UFRL; GB:AE007869; PIDN:AAK87127.1; PID:g15156391; GSPDB:  
C:Genetics:  
A:Gene: AGR\_C\_2462  
A:Map position: circular chromosome

Query Match  
Best Local Similarity 50.5%; Score 47; DB 2; Length 108;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AKYEAYKAAAAAPA 19  
Db 60 AAYEAYRARLADPA 74

## RESULT 6

AH2740  
conserved hypothetical protein Atu1336 [imported] - Agrobacterium tumefaciens (strain C5  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AH2740  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AH2740  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <KUR>  
A:Cross-references: UNIPROT:Q8UFRL; GB:AE008688; PIDN:AAL42342.1; PID:g17739747; GSPDB:  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu1336  
A:Map position: circular chromosome

Query Match  
Best Local Similarity 50.5%; Score 47; DB 2; Length 108;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AKYEAYKAAAAAPA 19  
Db 60 AAYEAYRARLADPA 74

## RESULT 7

QRMSE  
estrogen receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40061

R.White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.  
Mol. Endocrinol. 1, 735-744, 1987  
A>Title: Structural organization and expression of the mouse estrogen receptor.  
A/Reference number: A40061; MUID:91042558; PMID:2484714  
A/Accession: A40061  
A/Molecule type: mRNA  
A/Residues: 1-599 <WHI>  
A/Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180  
C/Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C/Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
C/Comment: complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C/Superfamily: estrogen receptor; erba transforming protein homology  
C/Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep  
F:1-183/Domain: amino-terminal <NH2>  
F:184-275/Domain: DNA binding #status predicted <DNA>  
F:187-460/Domain: erba transforming protein homology <ERBA>  
F:187-210/Region: zinc finger CCCC motif  
F:223-245/Region: zinc finger CCCC motif  
F:260-275/Region: nuclear location signal  
F:304-556/Domain: steroid binding #status predicted <STB>  
F:189,192,206,209/Binding site: zinc (Cys) #status predicted  
F:225,231,241,244/Binding site: zinc (Cys) #status predicted  
F:240,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 50.5%; Score 47; DB 1; Length 599;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 PEKAKYEAYKAAAPAA 19  
|||: ||| ||| |||  
Db 55 PEKAYEYFNAAAAA 72

RESULT 8  
F97683  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97683  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97683  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK8423.1; PID:g15157917; GSPDB:G  
C/Genetics:  
A/Map position: circular chromosome  
C/Superfamily: Escherichia coli ribosomal proteain L19

Query Match 49.5%; Score 46; DB 2; Length 179;  
Best Local Similarity 63.2%; Pred. No. 11;  
Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAPAA 19  
|||: ||| ||| |||  
Db 135 AEEKARLEAEKVAAQAALA 153

RESULT 9  
AF2908  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AF2908  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCIell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AF2908  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Map position: circular chromosome  
C/Superfamily: Escherichia coli ribosomal proteain L19

Query Match 49.5%; Score 46; DB 2; Length 179;  
Best Local Similarity 63.2%; Pred. No. 11;  
Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAPAA 19  
|||: ||| ||| |||  
Db 135 AEEKARLEAEKVAAQAALA 153

RESULT 10  
S39979  
chitinase (EC 3.2.1.14) - rice  
C/Species: Oryza sativa (rice)  
C/Date: 18-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C/Accession: S39979  
R/Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.  
Mol. Gen. Genet. 241, 1-10, 1993  
A>Title: Sequence variation, differential expression and chromosomal location of rice c  
A/Reference number: S39979; MUID:94049667; PMID:7901749  
A/Accession: S39979  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-339 <NIS>  
A/Cross-references: UNIPROT:Q43294; EMBL:X56787  
C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:33-74/Domain: hevein chitin-binding domain homology <HCB>  
F:91-329/Domain: plant chitinase homology <PCH>

Query Match 49.5%; Score 46; DB 2; Length 339;  
Best Local Similarity 76.9%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 YEAYKAAAPAA 19  
|||: ||| ||| |||  
Db 117 YEAFIAAAAFPA 129

RESULT 11  
S40414  
chitinase (EC 3.2.1.14) - rice  
C/Species: Oryza sativa (rice)  
C/Date: 25-Dec-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C/Accession: S40414  
R/Nishizawa, Y.  
submitted to the EMBL Data Library, November 1990  
A/Reference number: S40414  
A/Accession: S40414  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-340 <NIS>  
A/Cross-references: UNIPROT:Q43294; EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407  
C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:33-74/Domain: hevein chitin-binding domain homology <HCB>  
F:92-330/Domain: plant chitinase homology <PCH>

Query Match 49.5%; Score 46; DB 2; Length 340;

Best Local Similarity 76.9%; Pred. No. 20;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YEAYKAAAPAA 19  
| | | | | | | | | |  
Db 118 YEAFLLAAAPFA 130

## RESULT 12

T23177  
hypothetical protein K01D12.7 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T23177; T23188

R.Dobson, R.  
submitted to the EMBL Data Library, June 1996

A/Reference number: Z19703

A/Accession: T23177

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-84 <WIL>

A/Cross-references: UNIPROT:Q27223; UNIPROT:Q95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB:

A/Experimental source: clone K01D12

A/Accession: T23188

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-84 <W12>

A/Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CESP:K01D12.15

A/Experimental source: clone K01D12

C/Genetics:

A/Gene: CESP:K01D12.7; CESP:K01D12.15

A/Map position: 5

## Query Match

Best Local Similarity 48.4%; Score 45; DB 2; Length 84;

Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAPAA 19  
| | | | | | | | | |  
Db 34 PPKASASATKAAAPAPA 51

## RESULT 13

AB3271  
hypothetical protein BMEI0151 [imported] - *Brucella melitensis* (strain 16M)

C/Species: *Brucella melitensis*

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C/Accession: AB3271

R.DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leless

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*

A/Reference number: AD3252; PMID:11756688

A/Accession: AB3271

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-107 <KUR>

A/Cross-references: UNIPROT:Q8YJDS; GB:AE008917; PIDN:AAL51333.1; PID:gl7982031; GSPDB:G

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BMEI0151

A/Map position: 1

## Query Match

Best Local Similarity 48.4%; Score 45; DB 2; Length 107;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAPAA 18  
| | | | | | | | | |  
Db 57 PSLADYEAYRSRLAADP 73

## RESULT 14

## H81076

conserved hypothetical protein NMB1500 [imported] - *Neisseria meningitidis* (strain MC58

C/Species: *Neisseria meningitidis*

C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C/Accession: H81076

R.Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.,

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.

Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vc

A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A/Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: H81076

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-154 <TET>

A/Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:G7226737; PIDN:AAFA185

A/Experimental source: serogroup B, strain MC58

C/Genetics:

A/Gene: NMB1500

C/Superfamily: *Escherichia coli* ybdQ protein

Query Match 48.4%; Score 45; DB 2; Length 154;  
Best Local Similarity 56.2%; Pred. No. 13;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAPAA 16  
| | | | | | | | | |  
Db 48 APEFLQHESTYEAAPAA 63

## RESULT 15

B81866  
conserved hypothetical protein NMA1703 [imported] - *Neisseria meningitidis* (strain Z2491

C/Species: *Neisseria meningitidis*

C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C/Accession: B81866

R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: B81866

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-154 <PAR>

A/Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CAB8493

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA1703

C/Superfamily: *Escherichia coli* ybdQ protein

Query Match 48.4%; Score 45; DB 2; Length 154;  
Best Local Similarity 56.2%; Pred. No. 13;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAPAA 16  
| | | | | | | | | |  
Db 48 APEFLQHESTYEAAPAA 63

Search completed: February 26, 2005, 23:57:15  
Job time : 17.8673 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 82.5918 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-89  
Perfect score: 93  
Sequence: 1 APEKAKYEAYKAAAAAPA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	54	58.1	319	2 Q9N603	Q9N603 drosophila
2	54	58.1	319	2 Q9NG86	Q9NG86 drosophila
3	54	58.1	319	2 Q9NG87	Q9NG87 drosophila
4	54	58.1	319	2 Q9NG88	Q9NG88 drosophila
5	54	58.1	319	2 Q9NG89	Q9NG89 drosophila
6	54	58.1	319	2 Q9NG90	Q9NG90 drosophila
7	54	58.1	442	1 BNB DROME	P29746 drosophila
8	50	53.8	570	2 Q96M46	Q96M46 homo sapien
9	50	53.8	993	2 Q7S6Z8	Q7S6Z8 neurospora
10	49	52.7	641	2 Q05508	Q05508 trypanosoma
11	48	51.6	130	1 TAT_SIVM1	P05911 simian immu
12	48	51.6	300	2 Q9VFL4	Q9VFL4 drosophila
13	48	51.6	463	2 Q9V7U6	Q9V7U6 drosophila
14	48	51.6	707	2 Q64CP3	Q64CP3 uncultured
15	48	51.6	949	2 Q82KI6	Q82KI6 streptomyce
16	47	50.5	32	1 TAT_SIVM2	P05912 simian immu
17	47	50.5	106	1 TAT_SIVML	P11263 simian immu
18	47	50.5	108	2 Q8UFR1	Q8UFR1 agrobacteri
19	47	50.5	110	2 Q98DQ0	Q98DQ0 rhizobium 1
20	47	50.5	130	2 Q07390	Q07390 chimpanzee
21	47	50.5	130	2 Q88013	Q88013 chimpanzee
22	47	50.5	130	2 Q88070	Q88070 chimpanzee
23	47	50.5	131	1 TAT_SIVMK	P05910 simian immu
24	47	50.5	131	2 O11786	O11786 chimpanzee
25	47	50.5	131	2 Q07382	Q07382 chimpanzee
26	47	50.5	131	2 Q90EX2	Q90EX2 simian immu
27	47	50.5	131	2 Q90EX7	Q90EX7 simian immu
28	47	50.5	131	2 Q87708	Q87708 chimpanzee
29	47	50.5	131	2 Q88106	Q88106 chimpanzee
30	47	50.5	232	2 Q9ZTR8	Q9ZTR8 hordeum vul
31	47	50.5	315	2 Q9QNM5	Q9qnm5 sweet potat

32	47	50.5	315	2 Q9QNM8	Q9qnm8 sweet potat
33	47	50.5	375	2 Q75GC3	Q75GC3 oryza sativ
34	47	50.5	409	2 Q7ZXX5	Q7zxx5 xenopus lae
35	47	50.5	409	2 Q9DGF6	Q9dgf6 xenopus lae
36	47	50.5	599	1 ESRI_MOUSE	P19785 mus musculu
37	47	50.5	616	2 Q91D96	Q91d96 oryza sativ
38	47	50.5	753	2 Q62G40	Q62g40 burkholderi
39	47	50.5	753	2 Q63QD0	Q63qd0 burkholderi
40	46.5	50.0	131	2 Q6MAY0	Q6may0 paracitlamyd
41	46.5	50.0	300	2 Q729M4	Q729m4 desulfovibr
42	46	49.5	179	1 RL19_AGR75	Q8ubz5 agrobacteri
43	46	49.5	196	2 Q8K1A9	Q8K1a9 rhizobium e
44	46	49.5	200	2 P82166	P82166 locusta mig
45	46	49.5	236	1 H1_NEUCR	Q8j0u2 neurospora

## ALIGNMENTS

```
RESULT 1
Q9N603          PRELIMINARY;      PRT;      319 AA.
ID  Q9N603;
AC  Q9N603;
DT  01-OCT-2000 (TREMBlrel. 15, Created)
DT  01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Bangles and beads protein (Fragment).
GN  Name=bhb;
OS  Drosophila simulans (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7240;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sim5, Sim2, and Sim3;
RX  MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA  Begun D.J., Whitley P.;
RT  "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965 (2000).
DR  EMBL; AF256069; AAF68655.1; -.
DR  EMBL; AF256066; AAF68652.1; -.
DR  EMBL; AF256067; AAF68653.1; -.
DR  FlyBase; FBgn0041666; Dsim\bhb.
FT  NON TER.
SQ  SEQUENCE      319 AA;  33129 MW;  FEFB5ABD601C2B67 CRC64;

Query Match      58.1%; Score 54; DB 2; Length 319;
Best Local Similarity 63.2%; Pred. No. 6.9;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 APEKAKYEAYKAAAAAPA 19
Db      141 APEKKSIESPPAAAAASPA 159

RESULT 2
Q9NG86          PRELIMINARY;      PRT;      319 AA.
ID  Q9NG86;
AC  Q9NG86;
DT  01-OCT-2000 (TREMBlrel. 15, Created)
DT  01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT  01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE  Bangles and beads protein (Fragment).
GN  Name=bhb;
OS  Drosophila simulans (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7240;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sim8;
```

```

RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256072; AAF68658.1; -.
DR FlyBase; FBgn0041666; Dsim\bnb.
FT NON TER 1
SQ SEQUENCE 319 AA; 33169 MW; 0536BA5382A4AC47 CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 319;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAAAPA 19
Db 141 APEKKSIESSPAAAAASPA 159

RESULT 3
Q9NG87 PRELIMINARY; PRT; 319 AA.
AC Q9NG87;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=bnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim7;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256071; AAF68657.1; -.
DR FlyBase; FBgn0041666; Dsim\bnb.
FT NON TER 1
SQ SEQUENCE 319 AA; 33185 MW; B1178655BE5D662D CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 319;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAAAPA 19
Db 141 APEKKSIESSPAAAAASPA 159

RESULT 4
Q9NG88 PRELIMINARY; PRT; 319 AA.
AC Q9NG88;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=bnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim6;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";

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RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256070; AAF68656.1; -.
DR FlyBase; FBgn0041666; Dsim\bnb.
FT NON TER 1
SQ SEQUENCE 319 AA; 33165 MW; FC7BF5A566FDP9D2 CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 319;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAAAPA 19
Db 141 APEKKSIESSPAAAAASPA 159

RESULT 5
Q9NG89 PRELIMINARY; PRT; 319 AA.
AC Q9NG89;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=bnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim4;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256068; AAF68654.1; -.
DR FlyBase; FBgn0041666; Dsim\bnb.
FT NON TER 1
SQ SEQUENCE 319 AA; 33157 MW; A2020D5038CE7625 CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 319;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKYEAYKAAAAAPA 19
Db 141 APEKKSIESSPAAAAASPA 159

RESULT 6
Q9NG90 PRELIMINARY; PRT; 319 AA.
AC Q9NG90;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Bangles and beads protein (Fragment).
GN Name=bnb;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sim1;
RX MEDLINE=20283933; PubMed=10823947; DOI=10.1073/pnas.97.11.5960;
RA Begun D.J., Whitley P.;
RT "Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
DR EMBL; AF256065; AAF68651.1; -.
DR FlyBase; FBgn0041666; Dsim\bnb.

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FT  NON_TER      1      1
SQ  SEQUENCE      319 AA; 33157 MW; EDEED188E68F3B6F CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 319;
Matches 12; Conservativity 63.2%; Pred. No. 6.9;
                2; Mismatches 5; Indels 0; Gaps 0;

OY      1 APEKAKYEAYKAAAAAPA 19
      ||||| : |||||:
      141 APEKKSIESSPAAAAASPA 159

RESULT 7
BNB_DROME      STANDARD;      PRT;      442 AA.
ID  BNB_DROME
AC  P29746; Q9VWQ0;
DT  01-APR-1993 (Rel. 25, Created)
DT  01-APR-1993 (Rel. 25, Last sequence update)
DT  25-JAN-2005 (Rel. 46, Last annotation update)
DE  Bangles and beads protein.
GN  Name=bhb; ORFNames=CG7088;
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90126372; PubMed=2693037;
RA  Ng S.C., Perkins L.A., Conboy G., Perrimon N., Fishman M.C.;
RT  "A Drosophila gene expressed in the embryonic CNS shares one conserved
RL  domain with the mammalian GAP-43."
RN  [2]
RP  REVISIONS.
RX  MEDLINE=92201643; PubMed=1551578;
RA  Eberl D.F., Perkins L.A., Engelstein M., Hilliker A.J., Perrimon N.;
RT  "Genetic and developmental analysis of polytene section 17 of the X
RL  chromosome of Drosophila melanogaster."
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Berkeley;
RX  MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA  Fosler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nuskeirn D.R., Pacleb J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA  Williams S.M., Woodman T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster."
RL  Science 287:2185-2195 (2000).
RN  [4]
RP  GENOME REANNOTATION.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review."
RL  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Berkeley; TISSUE=Head;
RX  MEDLINE=22426066; PubMed=12537569;
RA  Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA  George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA  Rubin G.M., Celniker S.E.;
RT  "A Drosophila full-length cDNA resource."
RL  Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
CC  -1- FUNCTION: May play an important role during development.
CC  -1- TISSUE SPECIFICITY: Expressed in the embryonic CNS, in sets of
CC  cells that are segmentally reiterated along the periphery of the
CC  nervous system.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X63828; CAA45323.1; -
DR  EMBL; AE003510; AAF48888.1; -
DR  EMBL; AY060682; AAL28230.1; -
DR  PIR; A43555; A43555.
DR  FlyBase; FBgn0001090; bnb.
DR  GO; GO:007275; P:development; IMP.
DR  GO; GO:0042063; P:gliogenesis; IEP.
KW  Developmental protein.
SQ  SEQUENCE 442 AA; 45815 MW; 8EB67F77656A1200 CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 1; Length 442;
Matches 12; Conservativity 63.2%; Pred. No. 9.4;
                2; Mismatches 5; Indels 0; Gaps 0;

OY      1 APEKAKYEAYKAAAAAPA 19
      ||||| : |||||:
      264 APEKKSIESSPAAAAASPA 282

RESULT 8
ID  Q96M46      PRELIMINARY;      PRT;      570 AA.
AC  Q96M46;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Hypothetical protein FLJ32830.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obaayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
RA Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK057392; BAB71466.1; -.
DR InterPro; IPR008938; ARM.
SQ SEQUENCE 570 AA; 65769 MW; 65BEB6F244FC7E2 CRC64;

Query Match 53.8%; Score 50; DB 2; Length 570;
Best Local Similarity 69.2%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAA 14
Db 194 PEKAKYEAYRTLA 206

RESULT 9
Q7S6Z8 PRELIMINARY; PRT; 993 AA.
AC Q7S6Z8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Predicted protein.
GN Name=NCU05565.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-U., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thumann N., Barrett R., Gnerre S.,

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RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flammann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100321; EAA31291.1; -.
SQ SEQUENCE 993 AA; 107526 MW; 4A954861D16D763F CRC64;

Query Match 53.8%; Score 50; DB 2; Length 993;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAAP 18
Db 587 APEPTKKPAIPAAAAAP 604

RESULT 10
Q05508 PRELIMINARY; PRT; 641 AA.
AC Q05508;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Flagellum-Associated Protein (Fragment).
GN Name=FL-160-4;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL;
RX MEDLINE=93340646; PubMed=7688032;
RA Van Voorhis W.C., Barrett L., Koelling R., Farr A.G.;
RT "FL-160 proteins of Trypanosoma cruzi are expressed from a multigene
RT family and contain two distinct epitopes that mimic nervous tissues.";
RL J. Exp. Med. 178:681-694(1993).
DR EMBL; X70950; CAA50289.1; -.
DR PIR; PH1919; PH1919.
DR HSSP; O44049; INIT.
DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR008377; Sialidase-trypan.
DR PRINTS; PR01803; TCSIALIDASE.
FT NON TER 1
SQ SEQUENCE 641 AA; 68938 MW; 36C9928C010D5F4B CRC64;

Query Match 52.7%; Score 49; DB 2; Length 641;
Best Local Similarity 47.4%; Pred. No. 75;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAAPA 19
Db 376 SPEKSKNEKYSAGSGQAPS 394

RESULT 11
TAT_SIVM1 STANDARD; PRT; 130 AA.
AC P05911;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN Name=TAT;

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OS Simian immunodeficiency virus (Mm142-83 isolate) (SIV-MAC).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11733;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87287230; PubMed=3649576; DOI=10.1038/328543a0;
RA Chakrabarti L., Guyader M., Allison M., Daniel M.D., Desrosiers R.C.,
RA Tiollais P., Sonigo P.;
RT "Sequence of simian immunodeficiency virus from macaque and its
RT relationship to other human and simian retroviruses.";
RL Nature 328:543-547(1987);
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -1- SUBUNIT: Binds cyclin T1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -1- MISCELLANEOUS: This is a macaque isolate.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00277; CAB46521.1; -.
DR PIR; F28887; TNLJG3.
DR HSSP; P12506; 1TBC.
DR HIV; M16403; TAT$MM142.
DR InterPro; IPR001831; IV_Tac.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; AIDS; Nuclear protein; RNA-binding;
KW Transcription regulation.
SQ SEQUENCE 130 AA; 14545 MW; DA133BC4BAB7F521 CRC64;

Query Match          51.6%; Score 48; DB 1; Length 130;
Best Local Similarity 58.8%; Pred. No. 23;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 PEKAKYEAYKAAAAAP 18
Db 110 PKKAKKETVEAAVATAP 126

RESULT 12
O9VFL4 PRELIMINARY; PRT; 300 AA.
AC O9VFL4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE CG14840-PA(AT18408p).
GN ORFNames=CG14840;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabo G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FLYBase;
RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.

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RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003704; AAF55038.1; -.
DR EMBL; AY089356; AAL90094.1; -.
DR Intact; Q9VFL4; -.
DR FlyBase; FBgn0038217; CG14840.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;

Query Match          51.6%; Score 48; DB 2; Length 300;
Best Local Similarity 64.7%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAAPA 19
Db 242 EKTQAAAYKAACAAVEA 258

RESULT 13
O9V7U6 PRELIMINARY; PRT; 463 AA.
AC Q9V7U6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE CG6301-PA.
GN ORFNames=CG6301;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

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RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003805; AAF57947.2; -.
DR Intact; Q9V7U6; -.
DR FlyBase; FBgn0034161; CG6301.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEFB6EBC9 CRC64;

Query Match          51.6%; Score 48; DB 2; Length 463;
Best Local Similarity 64.7%; Pred. No. 78;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 EKAKYEAYKAAAAAPA 19
Db 275 EKTQAAAYKAACAAVEA 291

RESULT 14
O64CP3 PRELIMINARY; PRT; 707 AA.
AC O64CP3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=G21D1_21;

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OS uncultured archaeon GZfosID1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY714833; AAU82834.1; -
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match 51.6%; Score 48; DB 2; Length 707;
Best Local Similarity 70.6%; Pred. No. 1.2e+02;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEKAKYEAVYKAAAAA 17
   ||| ||| ||| ||| |||
DB 643 AAELKSEAERAAAAA 659

RESULT 15
Q82KI6 PRELIMINARY; PRT; 949 AA.
AC Q82KI6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV2417;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005030; BAC70128.1; -
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR003781; COA binding.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR Pfam; PF02629; COA_binding_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 949 AA; 100557 MW; 98B8E5ED93FCC9D3 CRC64;

Query Match 51.6%; Score 48; DB 2; Length 949;
Best Local Similarity 57.9%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY 1 APEKAKYEAVYKAAAAAPA 19
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DB 582 AADQALAEALRSAAAAAPA 600
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Search completed: February 26, 2005, 23:55:41  
Job time : 84.5918 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 86.9082 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-90  
Perfect score: 82  
Sequence: 1 EKAKYEAYKAAAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	17	5	ABP52296 HLA-DR2 m
2	82	100.0	19	5	ABP52295 HLA-DR2 m
3	71	86.6	15	5	ABP52271 HLA-DR2 m
4	71	86.6	15	5	ABP52298 HLA-DR2 m
5	71	86.6	17	5	ABP52294 HLA-DR2 m
6	65	79.3	15	5	ABP52270 HLA-DR2 m
7	63	76.8	15	5	ABP52301 HLA-DR2 m
8	62	75.6	17	5	ABP52303 HLA-DR2 m
9	61	74.4	15	5	ABP52291 HLA-DR2 m
10	61	74.4	15	5	ABP52263 HLA-DR2 m
11	60	73.2	15	5	ABP52272 HLA-DR2 m
12	59	72.0	15	5	ABP52259 HLA-DR2 m
13	59	72.0	15	5	ABP52257 HLA-DR2 m
14	58	70.7	17	5	ABP52302 HLA-DR2 m
15	57	69.5	15	5	ABP52297 HLA-DR2 m
16	56	68.3	15	5	ABP52253 HLA-DR2 m
17	56	68.3	15	5	ABP52251 HLA-DR2 m
18	56	68.3	15	5	ABP52239 HLA-DR2 m
19	55	67.1	15	5	ABP52290 HLA-DR2 m
20	55	67.1	15	5	ABP52261 HLA-DR2 m
21	55	67.1	15	5	ABP52244 HLA-DR2 m
22	55	67.1	15	5	ABP52292 HLA-DR2 m
23	55	67.1	15	5	ABP52269 HLA-DR2 m
24	55	67.1	15	5	ABP52262 HLA-DR2 m
25	54	65.9	15	5	ABP52264 HLA-DR2 m

26	54	65.9	15	5	ABP52267	Abp52267 HLA-DR2 m
27	54	65.9	15	5	ABP52236	Abp52236 HLA-DR2 m
28	53	64.6	15	5	ABP52299	Abp52299 HLA-DR2 m
29	52	63.4	15	5	ABP52265	Abp52265 HLA-DR2 m
30	51	62.2	15	5	ABP52254	Abp52254 HLA-DR2 m
31	51	62.2	15	5	ABP52255	Abp52255 HLA-DR2 m
32	51	62.2	15	5	ABP52240	Abp52240 HLA-DR2 m
33	51	62.2	15	5	ABP52241	Abp52241 HLA-DR2 m
34	51	62.2	15	5	ABP52304	Abp52304 HLA-DR2 m
35	51	62.2	15	5	ABP52248	Abp52248 HLA-DR2 m
36	51	62.2	15	5	ABP52249	Abp52249 HLA-DR2 m
37	50	61.0	15	5	ABP52232	Abp52232 HLA-DR2 m
38	50	61.0	15	5	ABP52268	Abp52268 HLA-DR2 m
39	50	61.0	15	5	ABP52231	Abp52231 HLA-DR2 m
40	49	59.8	15	5	ABP52235	Abp52235 HLA-DR2 m
41	49	59.8	15	5	ABP52250	Abp52250 HLA-DR2 m
42	48	58.5	15	3	AAY58982	Aay58982 Copeptide
43	48	58.5	15	3	AAY82074	Aay82074 MHC class
44	48	58.5	15	4	AAG63193	Aag63193 Peptide w
45	48	58.5	15	5	ABP52277	Abp52277 HLA-DR2 m

ALIGNMENTS

RESULT 1  
ABP52296  
ID ABP52296 standard; peptide; 17 AA.  
XX  
AC ABP52296;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.  
XX  
KW Human leukocyte antigen; HLA, major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN W0200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
DR  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autotransigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 82; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 EKAKYEAYKAAAAAPA 17  
DB 1 EKAKYEAYKAAAAAPA 17  
  
RESULT 2  
ABP52295  
ID ABP52295 standard; peptide; 19 AA.  
XX  
AC ABP52295;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:89.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autotransigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
XX invention

SQ Sequence 19 AA;  
  
Query Match 100.0%; Score 82; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 EKAKYEAYKAAAAAPA 17  
DB 3 EKAKYEAYKAAAAAPA 19  
  
RESULT 3  
ABP52271  
ID ABP52271 standard; peptide; 15 AA.  
XX  
AC ABP52271;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autotransigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 15 AA;  
  
Query Match 86.6%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 EKAKYEAYKAAAAAPA 15

Db 1 EKAKEYEAYKAAAAA 15

## RESULT 4

ABP52298 standard; peptide; 15 AA.

AC ABP52298;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:92.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 15 AA;

Query Match 86.6%; Score 71; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKEYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | |  
Db 1 EKAKEYEAYKAAAAA 15

RESULT 5  
ABP52294 standard; peptide; 17 AA.

XX ABP52294;

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:88.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

OS Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention

XX Sequence 17 AA;

Query Match 86.6%; Score 71; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKEYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
| | | | | | | | | | | | | | | | |  
Db 3 EKAKEYEAYKAAAAA 17

RESULT 6  
ABP52270 standard; peptide; 15 AA.

AC ABP52270;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:64.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX  
XX 01-AUG-2002.  
XX PD  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX PS Claim 28; Page 39; 54pp; English.  
XX  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX SQ Sequence 15 AA;  
SQ  
Query Match 79.3%; Score 65; DB 5; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.0013;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAAKYEAYKAAAAA 15  
RESULT 7  
ABP52301  
ID ABP52301 standard; peptide; 15 AA.  
XX  
AC ABP52301;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:95.  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX  
XX 01-AUG-2002.  
XX PD  
XX PF 24-JAN-2002; 2002WO-US002071.  
XX PR 24-JAN-2001; 2001US-0263569P.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Strominger JL, Fridkis-Hareli M;  
XX DR WPI; 2002-608439/65.  
XX  
XX PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX PS Claim 28; Page 39; 54pp; English.  
XX  
XX CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX SQ Sequence 15 AA;  
SQ  
Query Match 76.8%; Score 63; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0028;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAAKYEAYKAAAAA 15  
RESULT 8  
ABP52303  
ID ABP52303 standard; peptide; 17 AA.  
XX  
AC ABP52303;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX  
XX PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
XX  
Query Match 75.6%; Score 62; DB 5; Length 17;  
Best Local Similarity 86.7%; Pred. No. 0.0046;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
|||:|||||  
Db 3 EKAKFEAYKAAAAA 17  
XX  
RESULT 9  
ABP52291  
ID ABP52291 standard; peptide; 15 AA.  
XX  
AC ABP52291;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;

XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 74.4%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EKAKYEAYKAAAAA 15  
|||:|||||  
Db 1 EKPKYEAYKAAAAA 15  
XX  
RESULT 10  
ABP52263  
ID ABP52263 standard; peptide; 15 AA.  
XX  
AC ABP52263;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:57.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX Example 1; Page 33; 54pp; English.  
PS  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 74.4%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0058;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 EKAKEYEAYKAAAAA 15  
|:|||||  
Db 1 EAKKYEAYKAAAAA 15  
  
RESULT 11  
ABP52272  
ID ABP52272 standard; peptide; 15 AA.  
XX  
AC ABP52272;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:66.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 73.2%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0084;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Oy 1 EKAKEYEAYKAAAAA 15  
|:|||||  
Db 1 EAKKYEAYKAAAAA 15  
  
RESULT 12  
ABP52259  
ID ABP52259 standard; peptide; 15 AA.  
XX  
AC ABP52259;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:53.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Example 1; Page 33; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present  
invention  
XX  
SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.012;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKEYAYKAAAAA 15  
ID |||||  
AC 1 EKAAYAYKAAAAA 15

## RESULT 13

ABP52257  
ID ABP52257 standard; peptide; 15 AA.

XX ABP52257;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:51.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Example 1; Page 32; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.012;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKEYAYKAAAAA 15  
ID |||||  
DB 1 EKAAYAYKAAAAA 15

RESULT 14  
ABP52302  
ID ABP52302 standard; peptide; 17 AA.

XX ABP52302;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:96.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.  
OS Synthetic.

PN WO200259143-A2.

PD 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 17 AA;

Query Match 70.7%; Score 58; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.02;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKAKEYAYKAAAAA 15  
ID |||||  
DB 3 EKAKEYAYKAAAAA 17

RESULT 15  
ABP52297  
ID ABP52297 standard; peptide; 15 AA.  
XX  
AC ABP52297;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
OY 1 EKAKYEAYKAAAAA 15  
||:|||||||  
Db 1 EKPKEAYKAAAAA 15

Search completed: February 26, 2005, 23:48:23  
Job time : 87.9082 secs

Gencore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 22.7245 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-90  
Perfect score: 82  
Sequence: 1 EKAKYEAYKAAAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	54.9	1001	US-09-248-796A-18658	Sequence 18658, A
2	44.5	54.3	219	US-09-902-540-16623	Sequence 16623, A
3	44	53.7	405	US-09-328-352-4239	Sequence 4239, Ap
4	43	52.4	55	US-09-902-540-9849	Sequence 9849, Ap
5	43	52.4	172	US-09-902-540-13256	Sequence 13256, A
6	42	51.2	13	PCT-US95-04121-38	Sequence 38, App1
7	42	51.2	318	US-09-270-767-45996	Sequence 45996, A
8	41	50.0	102	US-09-101-751A-90	Sequence 90, App1
9	41	50.0	118	US-09-101-751A-46	Sequence 46, App1
10	41	50.0	218	US-09-101-751A-48	Sequence 48, App1
11	41	50.0	287	US-09-105-697-7	Sequence 7, App1
12	41	50.0	287	US-09-105-697-8	Sequence 8, App1
13	41	50.0	288	US-09-105-697-3	Sequence 3, App1
14	41	50.0	291	US-09-105-697-4	Sequence 4, App1
15	41	50.0	291	US-09-105-697-5	Sequence 5, App1
16	41	50.0	291	US-09-105-697-6	Sequence 6, App1
17	41	50.0	402	US-09-248-796A-17859	Sequence 17859, A
18	41	50.0	759	US-09-328-352-4241	Sequence 4241, Ap
19	41	50.0	830	US-07-977-434-6	Sequence 6, App1
20	41	50.0	830	US-08-458-819-6	Sequence 6, App1
21	41	50.0	830	PCT-US91-07035-6	Sequence 6, App1
22	41	50.0	831	US-08-073-384C-5	Sequence 5, App1
23	41	50.0	831	US-08-254-359A-5	Sequence 5, App1
24	41	50.0	831	US-08-483-043-5	Sequence 5, App1
25	41	50.0	831	US-08-481-238-5	Sequence 5, App1
26	41	50.0	831	US-08-471-0668-5	Sequence 5, App1
27	41	50.0	831	US-08-484-956-5	Sequence 5, App1

28	41	50.0	831	2	US-08-757-653-5	Sequence 5, App1
29	41	50.0	831	2	US-08-599-491-5	Sequence 5, App1
30	41	50.0	831	2	US-08-756-386-5	Sequence 5, App1
31	41	50.0	831	2	US-08-823-516-5	Sequence 5, App1
32	41	50.0	831	3	US-08-682-853A-5	Sequence 5, App1
33	41	50.0	831	3	US-08-759-038-5	Sequence 5, App1
34	41	50.0	831	3	US-08-758-314-5	Sequence 5, App1
35	41	50.0	831	3	US-09-350-309-5	Sequence 5, App1
36	41	50.0	831	3	US-08-520-946-5	Sequence 5, App1
37	41	50.0	831	4	US-09-684-938-5	Sequence 5, App1
38	41	50.0	831	4	US-09-308-825A-5	Sequence 5, App1
39	41	50.0	831	4	US-09-758-282B-5	Sequence 5, App1
40	41	50.0	831	4	US-09-655-378A-5	Sequence 5, App1
41	41	50.0	831	4	US-09-940-244-5	Sequence 5, App1
42	41	50.0	831	4	US-09-333-145-5	Sequence 5, App1
43	41	50.0	831	4	US-09-577-304A-5	Sequence 5, App1
44	41	50.0	832	4	US-09-758-282B-251	Sequence 251, App
45	41	50.0	832	4	US-09-758-282B-268	Sequence 268, App

ALIGNMENTS

RESULT 1  
US-09-248-796A-18658  
; Sequence 18658, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18658  
; LENGTH: 1001  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (21)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown  
US-09-248-796A-18658  
  
Query Match 54.9%; Score 45; DB 4; Length 1001;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 KAKYEAYKAAAAAPA 17  
Db 818 KAKEEAEAAAAAAA 833  
  
RESULT 2  
US-09-902-540-16623  
; Sequence 16623, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 16623  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-16623

Query Match 54.3%; Score 44.5; DB 4; Length 219;  
Best Local Similarity 70.6%; Pred. No. 8.9;  
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 EKAKEAYKAAAAAPA 17  
|||:|:|||||  
DB 191 EKARABT-EAAAAAPA 206

## RESULT 3

US-09-328-352-4239  
; Sequence 4239, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4239  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4239

Query Match 53.7%; Score 44; DB 4; Length 405;  
Best Local Similarity 66.7%; Pred. No. 21;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 AKYEAYKAAAAAPA 17  
||:|||||  
DB 81 AQFAGAGAAAAAPA 95

## RESULT 4

US-09-902-540-9849  
; Sequence 9849, Application US/09902540.  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 9849  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-9849

Query Match 52.4%; Score 43; DB 4; Length 55;  
Best Local Similarity 52.9%; Pred. No. 3.6;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKEAYKAAAAAPA 17  
||:|||||  
DB 2 ETAREQAYAEASACPA 18

## RESULT 5

US-09-902-540-13256  
; Sequence 13256, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13256  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13256

Query Match 52.4%; Score 43; DB 4; Length 172;  
Best Local Similarity 83.3%; Pred. No. 12;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 EAYKAAAAAPA 17  
|||:|||||  
DB 160 EAQKAKAAAAAPA 171

## RESULT 6

PCT-US95-04121-38  
; Sequence 38, Application PC/TUS9504121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof  
; NUMBER OF SEQUENCES: 62  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04121  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/222,206  
; FILING DATE: April 1, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vanstone, Darlene A.  
; REGISTRATION NUMBER: 35,279  
; REFERENCE/DOCKET NUMBER: 079.2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6010  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; PCT-US95-04121-38

Query Match 51.2%; Score 42; DB 5; Length 13;  
Best Local Similarity 76.9%; Pred. No. 1.1;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKYEAYKAAAAA 15

Db 1 AAYKAAKAAAAA 13

RESULT 7

US-09-270-767-45996  
; Sequence 45996, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Hdburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 45996  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-45996

Query Match 51.2%; Score 42; DB 4; Length 318;  
Best Local Similarity 61.5%; Pred. No. 34;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 YBAYKAAAAAPA 17  
Db 34 HPAKSGAASAPA 46

RESULT 8

US-09-101-751A-90  
; Sequence 90, Application US/09101751A  
; Patent No. 6465253  
; GENERAL INFORMATION:  
; APPLICANT: WICKHAM, THOMAS J.  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BROUGH, DOUGLAS E.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS.  
; FILE REFERENCE: 85710  
; CURRENT APPLICATION NUMBER: US/09/101,751A  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: WO 96US19150  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 08/700,846  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/701,124  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/563,368  
; PRIOR FILING DATE: 1995-11-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 90  
; LENGTH: 102;  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: ()..T)  
; OTHER INFORMATION: Description of Unknown Organism: Artificial  
; OTHER INFORMATION: Sequence  
US-09-101-751A-90

Query Match 50.0%; Score 41; DB 4; Length 102;  
Best Local Similarity 58.8%; Pred. No. 15;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKEAYKAAAAAPA 17  
Db 15 EKRAEAEAAAAAPA 31

RESULT 9  
US-09-101-751A-46  
; Sequence 46, Application US/09101751A  
; Patent No. 6465253  
; GENERAL INFORMATION:  
; APPLICANT: WICKHAM, THOMAS J.  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BROUGH, DOUGLAS E.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS  
; FILE REFERENCE: 85710  
; CURRENT APPLICATION NUMBER: US/09/101,751A  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: WO 96US19150  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 08/700,846  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/701,124  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/563,368  
; PRIOR FILING DATE: 1995-11-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: ()..T)  
; OTHER INFORMATION: Description of Unknown Organism: Artificial  
US-09-101-751A-46

Query Match 50.0%; Score 41; DB 4; Length 118;  
Best Local Similarity 58.8%; Pred. No. 17;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKEAYKAAAAAPA 17  
Db 19 EKRAEAEAAAAAPA 35

RESULT 10

US-09-101-751A-48  
; Sequence 48, Application US/09101751A  
; Patent No. 6465253  
; GENERAL INFORMATION:  
; APPLICANT: WICKHAM, THOMAS J.  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BROUGH, DOUGLAS E.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS  
; FILE REFERENCE: 85710  
; CURRENT APPLICATION NUMBER: US/09/101,751A  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: WO 96US19150  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 08/700,846  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/701,124  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/563,368  
; PRIOR FILING DATE: 1995-11-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 48  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: ()..T)  
; OTHER INFORMATION: Description of Unknown Organism: Artificial  
; OTHER INFORMATION: Sequence

US-09-101-751A-48

## Query Match

50.0%; Score 41; DB 4; Length 218;

Best Local Similarity 58.8%; Pred. No. 33;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAAPA 17

Db 19 EKRRAAEAAAEAAAAA 35

## RESULT 11

US-09-105-697-7

; Sequence 7, Application US/09105697

; Patent No. 6228628

; GENERAL INFORMATION:

; APPLICANT: Gelfand Ph.D., David H.

; APPLICANT: Reichert, Fred L.

; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Roche Molecular Systems

; STREET: 1080 U.S. Highway 202

; CITY: Branchburg

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 08876

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105,697

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Petry Ph.D., Douglas A.

; REGISTRATION NUMBER: 35321

; REFERENCE/DOCKET NUMBER: 1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 814-2974

; TELEFAX: (510) 814-2977

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 287 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-105-697-7

## Query Match

50.0%; Score 41; DB 3; Length 287;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAP 16

Db 75 YEAYKAGRAPTP 86

## RESULT 12

US-09-105-697-8

; Sequence 8, Application US/09105697

; Patent No. 6228628

; GENERAL INFORMATION:

; APPLICANT: Gelfand Ph.D., David H.

; APPLICANT: Reichert, Fred L.

; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Roche Molecular Systems

; STREET: 1080 U.S. Highway 202

; CITY: Branchburg

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 08876

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105,697

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Petry Ph.D., Douglas A.

; REGISTRATION NUMBER: 35321

; REFERENCE/DOCKET NUMBER: 1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 814-2974

; TELEFAX: (510) 814-2977

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 287 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-105-697-8

Query Match 50.0%; Score 41; DB 3; Length 287;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAP 16

Db 75 YEAYKAGRAPTP 86

## RESULT 13

US-09-105-697-3

; Sequence 3, Application US/09105697

; Patent No. 6228628

; GENERAL INFORMATION:

; APPLICANT: Gelfand Ph.D., David H.

; APPLICANT: Reichert, Fred L.

; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Roche Molecular Systems

; STREET: 1080 U.S. Highway 202

; CITY: Branchburg

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 08876

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105,697

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Petry Ph.D., Douglas A.

; REGISTRATION NUMBER: 35321

; REFERENCE/DOCKET NUMBER: 1043

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 814-2974

; TELEFAX: (510) 814-2977

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 288 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-105-697-3

Query Match 1 50.0%; Score 41; DB 3; Length 288;  
Best Local Similarity 66.7%; Pred. No. 44;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAP 16  
|||  
Db 77 YEAYKAGRAPTP 88

## RESULT 14

US-09-105-697-4  
; Sequence 4, Application US/09105697  
; Patent No. 6228628  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand Ph.D., David H.  
; APPLICANT: Reichert, Fred L.  
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Roche Molecular Systems  
; STREET: 1080 U.S. Highway 202  
; CITY: Branchburg  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08876  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,697  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry Ph.D., Douglas A.  
; REGISTRATION NUMBER: 35321  
; REFERENCE/DOCKET NUMBER: 1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 291 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-105-697-4

Query Match 1 50.0%; Score 41; DB 3; Length 291;  
Best Local Similarity 66.7%; Pred. No. 45;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAP 16  
|||  
Db 79 YEAYKAGRAPTP 90

## RESULT 15

US-09-105-697-5  
; Sequence 5, Application US/09105697  
; Patent No. 6228628  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand Ph.D., David H.  
; APPLICANT: Reichert, Fred L.  
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Roche Molecular Systems  
STREET: 1080 U.S. Highway 202  
CITY: Branchburg  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 08876  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,697  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry Ph.D., Douglas A.  
; REGISTRATION NUMBER: 35321  
; REFERENCE/DOCKET NUMBER: 1043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 291 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-105-697-5

Query Match 1 50.0%; Score 41; DB 3; Length 291;  
Best Local Similarity 66.7%; Pred. No. 45;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAP 16  
|||  
Db 79 YEAYKAGRAPTP 90

Search completed: February 26, 2005, 23:59:29  
Job time : 22.7245 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 : Search time 60.7143 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-90  
Perfect score: 82  
Sequence: 1 EKAKEYEAYKAAAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	17	US-10-056-583-90	Sequence 90, Appl
2	82	100.0	19	US-10-056-583-89	Sequence 89, Appl
3	71	86.6	15	US-10-056-583-65	Sequence 65, Appl
4	71	86.6	17	US-10-056-583-88	Sequence 88, Appl
5	65	79.3	15	US-10-056-583-64	Sequence 64, Appl
6	63	76.8	15	US-10-056-583-95	Sequence 95, Appl
7	62	75.6	15	US-10-056-583-92	Sequence 92, Appl
8	62	75.6	17	US-10-056-583-97	Sequence 97, Appl
9	61	74.4	15	US-10-056-583-57	Sequence 57, Appl
10	61	74.4	15	US-10-056-583-85	Sequence 85, Appl
11	60	73.2	15	US-10-056-583-66	Sequence 66, Appl
12	59	72.0	15	US-10-056-583-51	Sequence 51, Appl
13	59	72.0	15	US-10-056-583-53	Sequence 53, Appl

	14	58	70.7	17	14	US-10-056-583-96	Sequence 96, Appl
	15	57	69.5	15	14	US-10-056-583-91	Sequence 91, Appl
	16	56	68.3	15	14	US-10-056-583-33	Sequence 33, Appl
	17	56	68.3	15	14	US-10-056-583-45	Sequence 45, Appl
	18	56	68.3	15	14	US-10-056-583-47	Sequence 47, Appl
	19	55	67.1	15	14	US-10-056-583-38	Sequence 38, Appl
	20	55	67.1	15	14	US-10-056-583-55	Sequence 55, Appl
	21	55	67.1	15	14	US-10-056-583-56	Sequence 56, Appl
	22	55	67.1	15	14	US-10-056-583-63	Sequence 63, Appl
	23	55	67.1	15	14	US-10-056-583-84	Sequence 84, Appl
	24	55	67.1	15	14	US-10-056-583-86	Sequence 86, Appl
	25	54	65.9	15	14	US-10-056-583-30	Sequence 30, Appl
	26	54	65.9	15	14	US-10-056-583-58	Sequence 58, Appl
	27	54	65.9	15	14	US-10-056-583-61	Sequence 61, Appl
	28	53	64.6	15	14	US-10-056-583-93	Sequence 93, Appl
	29	52	63.4	15	14	US-10-056-583-59	Sequence 59, Appl
	30	51	62.2	15	14	US-10-056-583-34	Sequence 34, Appl
	31	51	62.2	15	14	US-10-056-583-35	Sequence 35, Appl
	32	51	62.2	15	14	US-10-056-583-42	Sequence 42, Appl
	33	51	62.2	15	14	US-10-056-583-43	Sequence 43, Appl
	34	51	62.2	15	14	US-10-056-583-48	Sequence 48, Appl
	35	51	62.2	15	14	US-10-056-583-49	Sequence 49, Appl
	36	51	62.2	15	14	US-10-056-583-98	Sequence 98, Appl
	37	50	61.0	15	14	US-10-056-583-25	Sequence 25, Appl
	38	50	61.0	15	14	US-10-056-583-26	Sequence 26, Appl
	39	50	61.0	15	14	US-10-056-583-62	Sequence 62, Appl
	40	49	59.8	15	14	US-10-056-583-29	Sequence 29, Appl
	41	49	59.8	15	14	US-10-056-583-44	Sequence 44, Appl
	42	48	58.5	15	9	US-09-765-301-19	Sequence 19, Appl
	43	48	58.5	15	10	US-09-765-644A-19	Sequence 19, Appl
	44	48	58.5	15	14	US-10-056-583-32	Sequence 32, Appl
	45	48	58.5	15	14	US-10-056-583-37	Sequence 37, Appl

## ALIGNMENTS

RESULT 1  
US-10-056-583-90  
; Sequence 90, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-90

Query Match 100.0%; Score 82; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKEYEAYKAAAAAPA 17  
Db 1 EKAKEYEAYKAAAAAPA 17

RESULT 2  
US-10-056-583-89

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; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

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Query Match          100.0%; Score 82; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAAPA 17
        |||||
Db       3 EKAKYEAYKAAAAAPA 19
```

```
RESULT 3
US-10-056-583-65;
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

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Query Match          86.6%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAAA 15
        |||||
Db       1 EKAKYEAYKAAAAAA 15
```

```
RESULT 4
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

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Query Match          86.6%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAAA 15
        |||||
Db       3 EKAKYEAYKAAAAAA 17
```

```
RESULT 5
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match          79.3%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 EKAKYEAYKAAAAAA 15
        |||||
Db       1 EAAKYEAYKAAAAAA 15
```

```
RESULT 6
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
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; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95
```

```
Query Match          76.8%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0025;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKYEAYKAAAAA 15
      |||||:|||||
Db      1 EKAKFEAFKAAAAA 15
```

## RESULT 7

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US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92
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```
Query Match          75.6%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0036;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKYEAYKAAAAA 15
      |||||:|||||
Db      1 EKAKYEAYKAAAAA 15
```

## RESULT 8

```
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match          75.6%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0041;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKYEAYKAAAAA 15
      |||||:|||||
Db      3 EKAKFEAYKAAAAA 17
```

## RESULT 9

```
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57
```

```
Query Match          74.4%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0051;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKYEAYKAAAAA 15
      |||||:|||||
Db      1 EKAKYAAAYKAAAAA 15
```

## RESULT 10

```
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-85

Query Match 74.4%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0051;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
DB 1 EKPKYEAYKAAAAA 15

RESULT 11  
US-10-056-583-66

; Sequence 66, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 73.2%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0074;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
DB 1 EAKKYEAYKAAAAA 15

RESULT 12  
US-10-056-583-51

; Sequence 51, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 72.0%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.011;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
DB 1 EAKRYAAYKAAAAA 15

RESULT 13  
US-10-056-583-53

; Sequence 53, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-53

Query Match 72.0%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.011;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
DB 1 EKAAYAYKAAAAA 15

RESULT 14  
US-10-056-583-96

; Sequence 96, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-96

Query Match 70.7%; Score 58; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.018;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | | | |  
DB 3 EKAKFEAYKAAAAA 17

```

RESULT 15
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack.L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

```

```

Query Match      69.5%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 EKAKYEAYKAAAAA 15
      ||:||:|||||
Db      1 EKPKFEAYKAAAAA 15

```

Search completed: February 27, 2005, 00:05:23  
 Job time : 60.7143 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:13:28 ; Search time 15.0918 Seconds  
(without alignments)  
108.382 Million cell updates/sec

Title: US-10-056-583A-90  
Perfect score: 82  
Sequence: 1 EKAKYEAYKAAAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	57.3	108	2	F97521 VCO33 protein homo
2	47	57.3	108	2	AH2740 conserved hypothet
3	46	56.1	339	2	S39979 chitinase (EC 3.2.
4	46	56.1	340	2	S40414 chitinase (EC 3.2.
5	45	54.9	188	2	I50145 homeotic protein H
6	45	54.9	289	2	A43562 homeotic protein H
7	44	53.7	270	2	T31225 traf protein homol
8	44	53.7	282	2	T51013 related to calmodu
9	44	53.7	398	2	T21061 hypothetical prote
10	44	53.7	503	1	VM071B variant surface gl
11	43	52.4	49	2	PX0029 protein C inhibito
12	43	52.4	176	2	G87606 transcripction regu
13	43	52.4	179	2	F97683 50S ribosomal prot
14	43	52.4	179	2	AF2908 50S ribosomal prot
15	43	52.4	185	2	S36290 T-cell receptor ga
16	43	52.4	379	2	T08277 carotenoid biosynt
17	43	52.4	441	2	A43555 GAP-43-related pro
18	43	52.4	736	2	D96830 probable heat-shoc
19	42	51.2	200	2	T48130 hypothetical prote
20	42	51.2	318	2	B48487 Moch (Tn4399) - Ba
21	42	51.2	698	2	T32594 hypothetical prote
22	42	51.2	748	2	S61247 DNA helicase/prima
23	42	51.2	2957	2	T33152 hypothetical prote
24	41.5	50.6	189	2	S77930 exoskeletal protei
25	41.5	50.6	189	2	S77935 exoskeletal protei
26	41	50.0	113	2	T30041 hypothetical prote
27	41	50.0	129	1	TNMG3 trans-activating t
28	41	50.0	165	2	B87702 ribosomal protein
29	41	50.0	168	2	T34804 hypothetical prote

30	41	50.0	177	2	AD1307 peptidyl methionin
31	41	50.0	177	2	AD1679 peptidyl methionin
32	41	50.0	192	1	MOCHLA myosin alkali ligh
33	41	50.0	254	2	H86355 probable 14-3-3 pr
34	41	50.0	421	2	JV0057 tola protein - Esc
35	41	50.0	470	2	AF2828 FAD dependent oxid
36	41	50.0	477	2	D97606 glycolate oxidase
37	41	50.0	521	2	T49355 related to protein
38	41	50.0	571	1	XZAD32 penton protein (II
39	41	50.0	571	1	XZADH5 penton protein (II
40	41	50.0	641	2	PH1919 FL-160-4 protein -
41	41	50.0	831	2	S26675 DNA-directed DNA p
42	41	50.0	1885	1	JC4086 fatty-acid synthas
43	41	50.0	2129	2	T27431 hypothetical prote
44	40.5	49.4	151	2	D87276 hypothetical prote
45	40.5	49.4	1655	2	T32633 hypothetical prote

ALIGNMENTS

RESULT 1  
F97521  
VCO33 protein homolog (AF179595) [imported] - Agrobacterium tumefaciens (strain C58, Ce  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97521  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97521  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-108 <KUR>  
A/Cross-references: UNIPROT:Q8UFR1; GB:AE007869; PIDN:AAK87127.1; PID:g15156391; GSPDB:  
C/Genetics:  
A/Map position: circular chromosome

Query Match 57.3%; Score 47; DB 2; Length 108;  
Best Local Similarity 66.7%; Pred. No. 2.6;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AKYEAYKAAAAAPA 17  
Db 60 AAYEAYRRLAADPA 74

RESULT 2  
AH2740  
conserved hypothetical protein Acu1336 [imported] - Agrobacterium tumefaciens (strain C  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AH2740  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AH2740  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-108 <KUR>  
A/Cross-references: UNIPROT:Q8UFR1; GB:AE008688; PIDN:AA142342.1; PID:g17739747; GSPDB:  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Map position: circular chromosome

Query Match 57.3%; Score 47; DB 2; Length 108;  
Best Local Similarity 66.7%; Pred. No. 2.6;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 3 AKYEAYKAAAAAPA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 60 AAYEAYRARLAADPA 74

RESULT 3  
S39979  
chitinase (EC 3.2.1.14) - rice  
C:Species: Oryza sativa (rice)  
C:Date: 18-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S39979  
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.  
Mol. Gen. Genet. 241, 1-10, 1993  
A:Title: Sequence variation, differential expression and chromosomal location of rice ch  
A:Reference number: S39979; MUID:94049667; PMID:7901749  
A:Accession: S39979  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-339 <NIS>  
A:Cross-references: UNIPROT:Q43294; EMBL:X56787  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:33-74/Domain: hevein chitin-binding domain homology <HCB>  
F:91-329/Domain: plant chitinase homology <PCH>

Query Match 56.1%; Score 46; DB 2; Length 339;  
Best Local Similarity 76.9%; Pred. No. 11;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 5 YEAYKAAAAAPA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 117 YEAFIAAAAAFPA 129

RESULT 4  
S40414  
chitinase (EC 3.2.1.14) - rice  
C:Species: Oryza sativa (rice)  
C:Date: 25-Dec-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S40414  
R:Nishizawa, Y.  
submitted to the EMBL Data Library, November 1990  
A:Reference number: S40414  
A:Accession: S40414  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-340 <NIS>  
A:Cross-references: UNIPROT:Q43294; EMBL:X56787; NID:9407471; PIDN:CAA40107.1; PID:94074  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:33-74/Domain: hevein chitin-binding domain homology <HCB>  
F:92-330/Domain: plant chitinase homology <PCH>

Query Match 56.1%; Score 46; DB 2; Length 340;  
Best Local Similarity 76.9%; Pred. No. 11;  
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 5 YEAYKAAAAAPA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 118 YEAFIAAAAAFPA 130

RESULT 5  
I50145  
homeotic protein Hox M - chicken  
N:Alternate names: CHOX M  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004

C:Accession: I50145; S14512  
R:Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.  
Leukemia 5, 357-360, 1991  
A:Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viru  
A:Reference number: I50145; MUID:9128215; PMID:1674560  
A:Accession: I50145  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-188 <CRO>  
A:Cross-references: UNIPROT:P23459; EMBL:X57158; NID:662700; PIDN:CAA40445.1; PID:662701  
C:Genetics:  
A:Gene: CHOX M  
C:Superfamily: homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:96-152/Domain: homeobox homology <HOX>

Query Match 54.9%; Score 45; DB 2; Length 188;  
Best Local Similarity 76.9%; Pred. No. 8.8;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 5 YEAYKAAAAAPA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 10 YSKYKAAAAAAA 22

RESULT 6  
A43562  
homeotic protein Hox D8 - mouse  
N:Alternate names: homeotic protein Hox 4.3  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: A43562  
R:Zipisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou  
Development 110, 733-745, 1990  
A:Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc  
A:Reference number: A43562; MUID:91209332; PMID:1982431  
A:Accession: A43562  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-289 <IZP>  
A:Cross-references: UNIPROT:P23463  
C:Superfamily: homeotic protein Hox A7; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:196-252/Domain: homeobox homology <HOX>

Query Match 54.9%; Score 45; DB 2; Length 289;  
Best Local Similarity 76.9%; Pred. No. 13;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 YEAYKAAAAAPA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 10 YSKYKAAAAAAA 22

RESULT 7  
T31225  
traf protein homolog - Spingomonas aromaticivorans plasmid pNL1  
C:Species: Spingomonas aromaticivorans  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T31225  
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; C  
submitted to the EMBL Data Library, July 1998  
A:Description: Complete sequence of a 184 kb catabolic plasmid from Spingomonas aromati  
A:Reference number: Z20992  
A:Accession: T31225  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-270 <ROM>  
A:Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:63378261; PID:63378366; PIDN:AAD  
C:Genetics:  
A:Genome: plasmid pNL1  
A>Note: traf

Query Match	53.7%;	Score 44;	DB 2;	Length 270;
Best Local Similarity	64.7%;	Pred. No. 18;		
Matches 11;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	EKAQYEAYKAAAAA	PA	17
Db	54	EKPKEEPRKAAAA	QPPA	70

RESULT 8  
T51013  
related to calmodulin-binding protein [imported] - *Neurospora crassa*  
N;Alternate names: protein B7J19.120  
C;Species: *Neurospora crassa*  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
C;Accession: T51013  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, July 2000  
A;Reference number: Z25286  
A;Accession: T51013  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-282 <SCH>  
A;Cross-references: EMBL:AL389899; GSPDB:GN00116; NCSP:B7J19.120  
A;Experimental source: BAC clone B7J19; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B7J19.120  
A;Map position: 6

Query Match	53.7%;	Score 44;	DB 2;	Length 282;
Best local Similarity	73.3%;	Pred. No. 18;		
Matches 11; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;
QY	3 AKYEAYKAAAAAPA	17		
	:			
DB	197 AKQKALAAAAAPA	211		

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RESULT 9
T21061
hypothetical protein F17C11.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21061
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19366
A:Accession: T21061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-398 <WIL>
A:Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDN:CAA96631.1; GSPDB:GN00023; CESP:FL
A:Experimental source: clone F17C11
C:Genetics:
A:Gene: CESP:F17C11.9
A:Map position: 5
A:Introns: 3/3; 44/3; 151/3; 196/1; 354/3
C:Superfamily: translation elongation factor eEF-1 gamma chain

Query Match          53.7%; Score 44; DB 2; Length 398;
Best Local Similarity 68.8%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1 EKAKYEAYKAAAAAP 16
      |||||
Db      214 EKPKEAKPAAAAAP 229

```

RESULT 10  
VMUT1B  
variant surface glycoprotein Antat 1.1 precursor - Trypanosoma brucei brucei  
C:Species: Trypanosoma brucei brucei  
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text\_change 09-Jul-2004

C/Accession: S07174; S18522; S09253; S10844  
R/Michiels, F.; Matchyskens, G.; Kronenberger, P.; Pays, E.; Dero, B.; van Assel, S.; D  
EMBO J. 2, 1185-1192, 1983  
A/Title: Gene activation and re-expression of a Trypanosoma brucei variant surface glyco  
A/Reference number: S07174; MUID:84028590; PMID:6313354  
A/Accession: S07174  
A/Molecule type: DNA  
A/Residues: 1-503 <MIC>  
A/Cross-references: UNIPROT:P06015; EMBL:X01843; NID:g10429; PIDN:CAA25971.1; PID:g1043  
A/Accession: S18522  
A/Molecule type: mRNA  
A/Residues: 1-503 <MIC2>  
A/Cross-references: GB:X01843; NID:g10429; PIDN:CAA25971.1; PID:g10430  
A/Note: part of this sequence, including the amino end of the mature protein, was confi  
R/van der Weff, A.; van Assel, S.; Aerts, D.; Steiner, M.; Pays, E.  
EMBO J. 9, 1035-1040, 1990  
A/Title: Telomere interactions may condition the programming of antigen expression in T  
A/Reference number: S09252; MUID:90214610; PMID:2323332

A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-333, 'P', 335-345, 'V', 347-416 <VAN>  
A;Cross-references: EMBL:X15817; NID:g10381; PIDN:CAA33809.1; PID:g10382  
R;Matthysens, G.; Michiels, F.; Hamers, R.; Pays, E.; Steinert, M.  
Nature 293, 230-233, 1981  
A;Title: Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-ter  
A;Reference number: A17609; MUID:82013622; PMID:7278981  
A;Accession: S10844  
A;Molecule type: mRNA  
A;Residues: 391-418, 'K', 420-503 <MATH>  
A;Cross-references: EMBL:J01213; NID:g162361; PIDN:AAA30280.1; PID:g162362  
A;Note: the authors translated the codon AAG for residue 419 as Asn and TTC for residue  
C;Superfamily: variant surface glycoprotein  
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-480/Product: variant surface glycoprotein AnTat 1.1 #status experimental <MAT>  
F;481-503/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;413, 419, 432/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;480/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature for

Query Match	53.7%	Score 44	DB 1	Length 503
Best Local Similarity	56.2%	Pred. No. 31		
Matches	9	Conservative	3	Mismatches 4; Indels 0; Gaps 0;
QY	1	EKAQYEAYKKA	AAAP	16
	:			:
DB	427	KKCKYNATKAS	SDAP	442

RESULT 11  
PX0029  
protein C inhibitor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: PX0029  
R:Suzuki, K.; Kusumoto, H.; Nishioka, J.; Komiyama, Y.  
J. Biochem. 107, 381-388, 1990  
A:Title: Bovine plasma protein C inhibitor with structural and functional homologous pro  
A:Reference number: PX0029; MUID:90256711; PMID:2160449  
A:Accession: PX0029  
A:Molecule type: protein  
A:Residues: 1-49 <SUZ>  
A:Cross-references: UNIPROT:Q9N2I2  
A:Experimental source: plasma  
C:Superfamily: Serpin

Query Match	52.4%	Score 43	DB 2	length 49
Best Local Similarity	61.5%	Pred. No. 5.2		
Matches	8	Conservative	3	Mismatches 2
				Indels 0
				Gaps 0
QY	5 YEAYKAAAAAPA	17		
	::: : : : :			
Db	27 FDLYRRLAAAAAPA	39		

## RESULT 12

G87606  
transcription regulator, AsnC family [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C/Accession: G87606  
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; MUID:21173698; PMID:11259647  
A/Accession: G87606  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-176 <STO>  
A/Cross-references: UNIPROT:Q9A4E7; GB:AE005673; NID:g13424505; PIDN:AAK24851.1; GSPDB:C  
C/Genetics:  
A/Gene: CC2887  
C/Superfamily: regulatory protein asnC

Query Match 52.4%; Score 43; DB 2; Length 176;  
Best Local Similarity 52.9%; Pred. No. 17;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAAPA 17  
|||: ||| ||| |||  
Db 99 EFARYEAFEAALVLRHPA 115

## RESULT 13

F97683  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97683  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97683  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:C  
C/Genetics:  
A/Gene: AGR\_C\_4900  
A/Map position: circular chromosome  
C/Superfamily: Escherichia coli ribosomal protein L19

Query Match 52.4%; Score 43; DB 2; Length 179;  
Best Local Similarity 64.7%; Pred. No. 17;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAAPA 17  
|||: ||| ||| |||  
Db 137 EKARLEAEKVAAAQALA 153

## RESULT 14

AF2908  
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AF2908  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mc Clell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AF2908  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-179 <KUR>  
A/Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAK43684.1; PID:g17741210; GSPDB:C  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: rplS  
A/Map position: circular chromosome  
C/Superfamily: Escherichia coli ribosomal protein L19

Query Match 52.4%; Score 43; DB 2; Length 179;  
Best Local Similarity 64.7%; Pred. No. 17;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAAAAPA 17  
|||: ||| ||| |||  
Db 137 EKARLEAEKVAAAQALA 153

## RESULT 15

S36290  
T-cell receptor gamma chain precursor - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C/Accession: S36290; S23041  
R/Hein, W.R.; Dudley, L.  
EMBO J. 12, 715-724, 1993  
A/Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta  
A/Reference number: S36287; MUID:93178447; PMID:8440261  
A/Accession: S36290  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-185 <HEI>  
A/Cross-references: EMBL:Z12998; NID:g2260; PIDN:CAA78342.1; PID:g2261  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 52.4%; Score 43; DB 2; Length 185;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EKAKYEAYKAAA 12  
: ||| ||| |||  
Db 81 DKAKYSYKGA 92

Search completed: February 26, 2005, 23:57:16  
Job time : 16.0918 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 73.898 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-90  
Perfect score: 82  
Sequence: 1 EKAKYEAYKAAAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	58.5	300	Q9VFL4	Q9VFL4 drosophila
2	48	58.5	463	Q9V7U6	Q9V7U6 drosophila
3	47	57.3	108	Q8UFR1	Q8UFR1 agrobacteri
4	47	57.3	110	Q9BDQ0	Q9BDQ0 rhizobium 1
5	46	56.1	340	Q43294	Q43294 oryza sativ
6	46	56.1	340	Q7DNA1	Q7DNA1 oryza sativ
7	45.5	55.5	457	Q94DE6	Q94DE6 oryza sativ
8	45	54.9	151	Q63KJ9	Q63KJ9 burkholderi
9	45	54.9	188	HXDB_CHICK	P23459 gallus gall
10	45	54.9	289	HXDB_MOUSE	P23463 mus musculu
11	45	54.9	289	Q8IXZ1	Q8IXZ1 homo sapien
12	45	54.9	290	HXDB_HUMAN	P13378 homo sapien
13	45	54.9	707	Q64CF3	Q64CF3 uncultured
14	45	54.9	949	Q82K16	Q82K16 streptomyce
15	44	53.7	71	Q9M3P6	Q9M3P6 hordeum mar
16	44	53.7	71	Q9M3Q7	Q9M3Q7 hordeum mur
17	44	53.7	158	Q84YW5	Q84YW5 oryza sativ
18	44	53.7	232	Q942W3	Q942W3 oryza sativ
19	44	53.7	270	Q85933	Q85933 sphingomona
20	44	53.7	274	Q8T4I3	Q8T4I3 drosophila
21	44	53.7	274	Q9VFL3	Q9VFL3 drosophila
22	44	53.7	282	Q7SCA9	Q7SCA9 neurospora
23	44	53.7	299	Q6YSU4	Q6YSU4 oryza sativ
24	44	53.7	356	Q6Z4U1	Q6Z4U1 oryza sativ
25	44	53.7	373	Q814K9	Q814K9 caenorhabdi
26	44	53.7	398	EF1G_CAEEL	P54412 caenorhabdi
27	44	53.7	403	Q7NZ81	Q7NZ81 chromobacte
28	44	53.7	503	VSA1_TRYBB	P06015 trypanosoma
29	44	53.7	677	Q64NT8	Q64NT8 bacteroides
30	43	52.4	71	Q9M3Q4	Q9M3Q4 hordeum bul
31	43	52.4	71	Q9M3Q6	Q9M3Q6 hordeum mur

32	43	52.4	176	2	Q9A4E7	Q9A4E7 caulobacter
33	43	52.4	177	1	RL19_RHIME	Q92139 rhizobium m
34	43	52.4	179	1	RL19_AGR75	Q8ub25 agrobacteri
35	43	52.4	181	1	RL19_RH110	P58168 rhizobium 1
36	43	52.4	220	2	Q70M24	Q70m24 halorubrum
37	43	52.4	223	2	Q70M29	Q70m29 halobacteri
38	43	52.4	225	2	Q70M27	Q70m27 halobacteri
39	43	52.4	227	2	Q67MU5	Q67mu5 symbiobacte
40	43	52.4	232	2	Q9ZTR8	Q9ztr8 hordeum vul
41	43	52.4	241	2	Q91ZP6	Q91zpe m nedda ww
42	43	52.4	241	2	Q8BVC5	Q8bvc5 mus musculu
43	43	52.4	241	2	Q61R02	Q61r02 mus musculu
44	43	52.4	299	1	RL22_DROME	P50887 drosophila
45	43	52.4	312	2	Q9UAN1	Q9uan1 drosophila

## ALIGNMENTS

RESULT 1  
Q9VFL4 PRELIMINARY; PRT; 300 AA.  
ID Q9VFL4  
AC Q9VFL4;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE CG14840-PA (AT18408p).  
GN ORFNames=CG14840;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mileshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";

```

RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Betman B.P.,
RA Beltercourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003704; AAF55038.1; -
DR EMBL; AY089356; AAL90094.1; -
DR Intact; Q9VFL4; -
DR FlyBase; FBgn0038217; CG14840.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;

Query Match 58.5%; Score 48; DB 2; Length 300;
Best Local Similarity 64.7%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAPAA 17
DB 242 EKTQAAAYKAACAVEA 258

RESULT 2
Q9V7U6 PRELIMINARY; PRT; 463 AA.
AC Q9V7U6;

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DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE CG6301-PA.
GN ORFNames=CG6301;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaverl J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]

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RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
 Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,  
 Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 Lewis S.E.,  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review."  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003805; AAF57947.2; -.  
 DR InAct; Q9V7U6; -.  
 DR FlyBase; FBgn0034161; CG6301.  
 DR InterPro; IPR007999; DUF745.  
 DR Pfam; PF05335; DUF745; 1.  
 SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEFB6BC9 CRC64;

Query Match 58.5%; Score 48; DB 2; Length 463;  
 Best Local Similarity 64.7%; Pred. No. 42;  
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 EKAKYAYKAAAAAPA 17  
 |||||  
 DB 275 ETKQAAYKAAACAVEA 291

## RESULT 3

Q8UFRI ..PRELIMINARY; PRT; 108 AA.  
 AC Q8UFRI; Q7CZH4;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein Atu1336 (AGR\_C\_2462p).  
 GN OrderedLocusNames=AGR\_C\_2462, Atu1336;  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dupont;  
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr.,  
 Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 Neeter E.W.,  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 C58."  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Cereon;  
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 RA Planagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.,  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 Agrobacterium tumefaciens C58."  
 RL Science 294:2323-2328(2001).  
 DR EMBL; AE009095; AAL42342.1; -.  
 DR EMBL; AE008059; AAK87127.1; -.  
 DR PIR; AH2740; AH2740.  
 DR PIR; F97521; F97521.  
 DR InterPro; IPR011008; Dimer A\_B\_barrel.  
 DR InterPro; IPR009478; DUF1059.  
 DR Pfam; PF06499; DUF1099; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 108 AA; 12371 MW; A48C7CB4BC22BD3A CRC64;

Query Match 57.3%; Score 47; DB 2; Length 108;  
 Best Local Similarity 66.7%; Pred. No. 16;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKYAYKAAAAAPA 17  
 |||||  
 DB 60 AAYEAYRRLAADPA 74

## RESULT 4

Q9BDQ0 ..PRELIMINARY; PRT; 110 AA.  
 AC Q9BDQ0;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE M14604 protein.  
 GN OrderedLocusNames=m14604;  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 Takeuchi C., Yamada M., Tabata S.,  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003004; BAB51220.1; -.  
 DR InterPro; IPR009478; DUF1099.  
 DR Pfam; PF06499; DUF1099; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 110 AA; 12441 MW; F41F0DDE3CA8885 CRC64;

Query Match 57.3%; Score 47; DB 2; Length 110;  
 Best Local Similarity 66.7%; Pred. No. 16;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKYAYKAAAAAPA 17  
 |||||  
 DB 61 AAYEAYRRLAADPA 75

## RESULT 5

Q43294 ..PRELIMINARY; PRT; 340 AA.  
 AC Q43294;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Chitinase precursor (EC 3.2.1.14).

```

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=japonica;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes.";
RL Mol. Gen. Genet. 241:1-10(1993).
DR EMBL; X56787; CAA40107.1; -.
DR PIR; S39979; S39979.
DR PIR; S40414; S40414.
DR HSSP; P23951; ICNS.
DR Gramene; Q43294; -.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_bind_1; 1.
DR PRINTS; PR00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChEBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
DR Chitin-binding; Glycosidase; Hydrolase; Signal.
KW Chitin-binding; Glycosidase; Potential.
FT SIGNAL 1 32 chitinase.
FT CHAIN 33 340
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 56.1%; Score 46; DB 2; Length 340;
Best Local Similarity 76.9%; Pred. No. 65;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAAPA 17
Db 118 YEAFLLAAAAAPPA 130

RESULT 6
Q7DNA1 PRELIMINARY; PRT; 340 AA.
AC Q7DNA1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Endochitinase precursor (EC 3.2.1.14).
GN Name=Chit-2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes.";
RL Mol. Gen. Genet. 241:1-10(1993).
DR EMBL; D16222; BAA03750.1; -.

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DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChEBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
DR Chitin-binding; Glycosidase; Hydrolase; Signal.
KW Chitin-binding; Glycosidase; Potential.
FT SIGNAL 1 32 endochitinase.
FT CHAIN 33 340
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 56.1%; Score 46; DB 2; Length 340;
Best Local Similarity 76.9%; Pred. No. 65;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAAPA 17
Db 118 YEAFLLAAAAAPPA 130

RESULT 7
Q94DE6 PRELIMINARY; PRT; 457 AA.
AC Q94DE6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative 3-deoxy-d-manno-octulosonic-acid transferase (KDO
transferase).
GN Name=P0683F02.6; Synonyms=OJ1402.H07.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.;
RA "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003289; BAB63703.1; -.
DR EMBL; AP003415; BAC03325.1; -.
DR Gramene; Q94DE6; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

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DR InterPro: IPR007507; Glycos transf\_N.  
DR Pfam: PF04413; Glycos\_transf\_N; 1.  
KW Transferase.  
SQ SEQUENCE 457 AA; 50371 MW; BEBC6C58CB86A4D1 CRC64;  
Query Match 55.5%; Score 45.5; DB 2; Length 457;  
Best Local Similarity 64.7%; Pred. No. 1e+02;  
Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;  
QY 2 KAKYEAYKAAA-AAAPA 17  
DB 15 RALYELYRAASRAAPA 31  
RESULT 8  
Q63KJ9 PRELIMINARY; PRT; 151 AA.  
AC Q63KJ9;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Putative exported protein.  
GN ORFNames=BHSS1363;  
OS Burkholderia pseudomallei K96243.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia.  
OX NCBI\_TaxID=272560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K96243;  
RX PubMed=15377794;  
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,  
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,  
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,  
RA Brooks K., Brown K.A., Brown N.F., Chailis G.L., Cherevach I.,  
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,  
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,  
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,  
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,  
RA Songshivai S., Stevens K., Tumapa S., Vesaratchaveest M.,  
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,  
RT "Genomic plasticity of the causative agent of melioidosis,  
RT Burkholderia pseudomallei";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).  
DR EMBL; BX571966; CAH3834.1; -.  
SQ SEQUENCE 151 AA; 14873 MW; 532610BF64B35F17 CRC64;  
Query Match 54.9%; Score 45; DB 2; Length 151;  
Best Local Similarity 68.8%; Pred. No. 44;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2 KAKYEAYKAAA-AAAPA 17  
DB 60 KTWYGASKAAAATAPA 75  
RESULT 9  
HXD8\_CHICK STANDARD; PRT; 188 AA.  
ID HXD8\_CHICK  
AC P23459;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-D8 (Hox-M).  
GN Name=HoxD8; Synonyms=CHOX-M;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT MEDLINE=91238215; PubMed=1674560;  
RX

RA Crompton M.R., McGregor A.D., Goodwin G.H.;  
RT "cDNA cloning of a homeobox-containing gene expressed in avian  
RT myeloblastic virus-transformed chicken monoblastic leukaemia cells.";  
RL Leukemia 5:357-360(1991).  
CC -1- FUNCTION: Sequence-specific transcription factor which is part of  
CC a developmental regulatory system that provides cells with  
CC specific positional identities on the anterior-posterior axis.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: Belongs to the Antp homeobox family.  
CC -1- SIMILARITY: Contains 1 homeobox domain.  
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-----  
DR EMBL; X57158; CAA40445.1; -.  
DR PIR; I50145; I50145.  
DR HSSP; P02833; 9ANT.  
DR TRANSFAC; T01754; -.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR009057; Homeobox.  
DR InterPro; IPR000047; HTH\_lambdarepressr.  
DR Pfam; PF00046; Homeobox\_1.  
DR PRINTS; PR00025; ANTENNAPEDIA.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;  
KW Transcription regulation.  
FT DOMAIN 15 25 Poly-Ala.  
FT SITE 83 88 Antp-type hexapeptide.  
FT DNA BIND 95 154 Homeobox.  
SQ SEQUENCE 188 AA; 21729 MW; D4560E8807FE29FE CRC64;  
Query Match 54.9%; Score 45; DB 1; Length 188;  
Best Local Similarity 76.9%; Pred. No. 53;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5 YEAYKAAA-AAAPA 17  
DB 10 YSKYKAAA-AAAA 22  
RESULT 10  
HXD8\_MOUSE STANDARD; PRT; 289 AA.  
ID HXD8\_MOUSE  
AC P23463;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Homeobox protein Hox-D8 (Hox-4.3) (Hox-5.4).  
GN Name=Hoxd8; Synonyms=Hox-4.3, Hoxd-8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91209232; PubMed=1982431;  
RA Izpisua-Belmonte J.-C., Dolle P., Renucci A., Zappavigna V.,  
RA Falkenstein H., Duboule D.;  
RT "Primary structure and embryonic expression pattern of the mouse Hox-  
RT 4.3 homeobox gene.";  
RL Development 110:733-745(1990).  
RX

```

RN [2]
RP SEQUENCE OF 191-289 FROM N.A.
RX MEDLINE=91274361; PubMed=1675873; DOI=10.1016/0167-4781(91)90020-M;
RA Sadoul R., Featherstone M.;
RT "Sequence analysis of the homeobox-containing exon of the murine Hox-
RL 4.3 homeogene.";
RN Blochim. Biophys. Acta 1089:259-261(1991).
RN [3]
RP SEQUENCE OF 195-254 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
RN [4]
RP SEQUENCE OF 192-260 FROM N.A.
RX MEDLINE=92212934; PubMed=1348361;
RA Nazareli A., Kim Y., Nirenberg M.;
RT "Hox-1.11 and Hox-4.9 homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR EMBL; X56561; CAA39911.1; -.
DR EMBL; M87803; AAA37852.1; -.
DR PIR; A43562; A43562.
DR PIR; S16177; A41605.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T01426; -.
DR MGD; MGI:96209; Hoxd8.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeoboxdomain_1like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 28 Poly-Ala.
FT DOMAIN 62 89 Gly/Pro-rich.
FT DOMAIN 108 117 Poly-Pro.
FT SITE 183 188 Antp-type hexapeptide.
FT DNA_BIND 195 254 Homeobox.
FT CONFLICT 207 208 TL -> RV (in Ref. 1).
FT CONFLICT 231 231 T -> S (in Ref. 1).
FT CONFLICT 265 266 EA -> DG (in Ref. 1).
FT CONFLICT 275 275 A -> V (in Ref. 2).
SQ SEQUENCE 289 AA; 31410 MW; 5783099FB9B2BDFE CRC64;
Query Match 54.9%; Score 45; DB 1; Length 289;
Best Local Similarity 76.9%; Pred. No. 80;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 YEAYKAAAPAA 17
DB 10 YSKYKAAAAAAA 22

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RESULT 11
Q8IXZ1 PRELIMINARY; PRT; 289 AA.
ID Q8IXZ1
AC Q8IXZ1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Homeo box D8.
GN Name=HOXD8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; BC038709; AAH38709.1; -.
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeoboxdomain_1like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 289 AA; 31839 MW; 4C2621085174B447 CRC64;
Query Match 54.9%; Score 45; DB 2; Length 289;
Best Local Similarity 76.9%; Pred. No. 80;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 YEAYKAAAPAA 17
DB 10 YSKYKAAAAAAA 22

```

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RESULT 12
HXD8_HUMAN STANDARD; PRT; 290 AA.
ID HXD8_HUMAN STANDARD; PRT; 290 AA.
AC P13378;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4).
GN Name=HOXD8; Synonyms=HOX4E;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Birren B., Linton L., Nusbaum C., Lander E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
RT "A complete mutation analysis panel of human HOX genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 193-287 FROM N.A.
RX MEDLINE=89306602; PubMed=2568311;
RA Oliver G., Sidel N., Fiske N., Heinzmann C., Mohandas T.,
RA Sparkes R.S., de Robertis E.M.;
RT "Complementary homeo protein gradients in developing limb buds.";
RL Genes Dev. 3:641-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR EMBL; AC009336; -; NOT ANNOTATED_CDS.
DR EMBL; AY014304; AAG42152.1; -.
DR EMBL; AY014303; AAG42152.1; JOINED.
DR EMBL; X15507; CAA33529.1; -.
DR PIR; B32830; B32830.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T03332; -.
DR Genew; HGNC:5139; HOXD8.
DR MIM; 142985; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeoboxdomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 15 23 Poly-Ala.
FT DOMAIN 45 50 Poly-Ala.
FT DOMAIN 109 123 Poly-Pro.

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FT DNA BIND 197 256 Homeobox.
FT CONFLICT 287 287 G -> A (in Ref. 3).
SQ SEQUENCE 290 AA; 31910 MW; 75FF95A73E2AA85F CRC64;

Query Match
Best Local Similarity 76.9%; Score 45; DB 1; Length 290;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YEAYKAAAAAAPA 17
DB 10 YSKYKAAAAAAA 22

RESULT 13
Q64CP3 PRELIMINARY; PRT; 707 AA.
AC Q64CP3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ1D1_21;
OS uncultured archaeon GZfos1D1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN (2)
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY174833; AAU82834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match
Best Local Similarity 73.3%; Score 45; DB 2; Length 707;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAA 15
DB 645 EKUKSEAEERAAAAA 659

RESULT 14
Q82KI6 PRELIMINARY; PRT; 949 AA.
AC Q82KI6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=SAV2417;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";

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Search completed: February 26, 2005, 23:55:43  
Job time : 75.898 secs

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RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005030; BAC70128.1; -
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR003781; CoA_binding.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR Pfam; PF02629; CoA_binding; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 949 AA; 100557 MW; 98B8E5ED93FCC9D3 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 949;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKYEAYKAAAAAPA 17
Db 584 DQALAEALRSAAAAAPA 600

RESULT 15
Q9M3P6 PRELIMINARY; PRT; 71 AA.
AC Q9M3P6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chitinase (Fragment).
GN Name=CHI;
OS Hordeum marinum subsp. marinum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=112516;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21957723; PubMed=11962631; DOI=10.1139/g01-158;
RT "Species relationships between antifungal chitinase and nuclear rDNA
RT (internal transcribed spacer) sequences in the genus Hordeum.";
RL Genome 45:339-347(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA de Bustos A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400142; CAB77517.1; -.
DR HSSP; P23951; 2BAA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 71 AA; 7724 MW; 5D6B896310B4C44C CRC64;

Query Match 53.7%; Score 44; DB 2; Length 71;
Best Local Similarity 64.3%; Pred. No. 31;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 KYEAYKAAAAAPA 17
Db 15 KYDAFLAAVAAPFA 28
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OM protein - protein search, using sw model

Run on: February 26, 2005, 23:06:18 ; Search time 86.9082 Seconds  
(without alignments)  
75.654 Million cell updates/sec

Title: US-10-056-583A-97  
Perfect score: 84  
Sequence: 1 APEKAKEAYKAAAPPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	17	5	ABP52303 HLA-DR2 m
2	80	95.2	17	5	ABP52302 HLA-DR2 m
3	73	86.9	17	5	ABP52294 HLA-DR2 m
4	73	86.9	19	5	ABP52295 HLA-DR2 m
5	68	81.0	15	5	ABP52297 HLA-DR2 m
6	65	77.4	15	5	ABP52291 HLA-DR2 m
7	62	73.8	15	5	ABP52271 HLA-DR2 m
8	62	73.8	15	5	ABP52298 HLA-DR2 m
9	62	73.8	15	5	ABP52304 HLA-DR2 m
10	62	73.8	17	5	ABP52296 HLA-DR2 m
11	61	72.6	15	5	ABP52301 HLA-DR2 m
12	61	72.6	15	5	ABP52299 HLA-DR2 m
13	59	70.2	15	5	ABP52290 HLA-DR2 m
14	59	70.2	15	5	ABP52292 HLA-DR2 m
15	56	66.7	15	5	ABP52270 HLA-DR2 m
16	55	65.5	15	5	ABP52300 HLA-DR2 m
17	55	65.5	15	5	ABP52305 HLA-DR2 m
18	52	61.9	15	5	ABP52263 HLA-DR2 m
19	51	60.7	15	5	ABP52272 HLA-DR2 m
20	51	60.7	572	4	ABB59072 Drosophila
21	50	59.5	15	5	ABP52259 HLA-DR2 m
22	50	59.5	15	5	ABP52257 HLA-DR2 m
23	49	58.3	15	5	ABP52289 HLA-DR2 m
24	47	56.0	15	5	ABP52253 HLA-DR2 m
25	47	56.0	15	5	ABP52251 HLA-DR2 m

26	47	56.0	15	5	ABP52239	Abp52239 HLA-DR2 m
27	46	54.8	15	5	ABP52261	Abp52261 HLA-DR2 m
28	46	54.8	15	5	ABP52244	Abp52244 HLA-DR2 m
29	46	54.8	15	5	ABP52269	Abp52269 HLA-DR2 m
30	46	54.8	15	5	ABP52262	Abp52262 HLA-DR2 m
31	46	54.8	570	6	ADA5549	Ada5549 Human pro
32	46	54.8	570	7	ADJ70708	Adj70708 Human hea
33	45	53.6	15	5	ABP52293	Abp52293 HLA-DR2 m
34	45	53.6	15	5	ABP52264	Abp52264 HLA-DR2 m
35	45	53.6	15	5	ABP52267	Abp52267 HLA-DR2 m
36	45	53.6	15	5	ABP52236	Abp52236 HLA-DR2 m
37	45	53.6	145	3	AAAB32749	Abb32749 Euca1yptu
38	45	53.6	203	8	ADS30243	Adbs30243 Bacterial
39	45	53.6	781	8	ADN60395	Adn60395 B. lichen
40	45	53.6	781	8	ADN60505	Adn60505 B. lichen
41	45	53.6	781	8	ADN60519	Adn60519 B. lichen
42	44	52.4	21	2	AAW19062	Aaw19062 Trypanoso
43	44	52.4	21	2	AAW19087	Aaw19087 Trypanoso
44	44	52.4	21	2	AAV32839	Aay32839 TCE repea
45	44	52.4	21	2	AAV33311	Aay33311 Epitope o

ALIGNMENTS

RESULT 1					
ABP52303	ABP52303 standard; peptide; 17 AA.				
ID	ABP52303;				
XX					
AC	ABP52303;				
XX					
DT	16-OCT-2002 (first entry)				
XX					
DE	HLA-DR2 molecule binding peptide SEQ ID NO:97.				
XX					
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
PN	WO200259143-A2.				
XX					
PD	01-AUG-2002.				
XX					
PF	24-JAN-2002; 2002WO-US002071.				
XX					
PR	24-JAN-2001; 2001US-0263569P.				
XX					
PA	(HARD ) HARVARD COLLEGE.				
XX					
PI	Strominger JL, Fridkis-Hareli M;				
XX					
DR	WPI; 2002-608439/65.				
XX					
PT	New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.				
PT					
XX					
PS	Claim 28; Page 39; 54pp; English.				
XX					
CC	The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases				

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
  
Query Match 100.0%; Score 84; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 APEKAKFEAYKAAAPAA 17  
Db 1 APEKAKFEAYKAAAPAA 17  
  
RESULT 2  
ABP52302  
ID ABP52302 standard; peptide; 17 AA.  
XX  
AC ABP52302;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX

SQ Sequence 17 AA;  
  
Query Match 95.2%; Score 80; DB 5; Length 17;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 APEKAKFEAYKAAAPAA 17  
Db 1 APEKAKFEAYKAAAPAA 17  
  
RESULT 3  
ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 AA;  
  
Query Match 86.9%; Score 73; DB 5; Length 17;  
Best Local Similarity 88.2%; Pred. No. 5.9e-05;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 APEKAKFEAYKAAAPAA 17

```
Db      1 APEKAKYEAYKAAAAA 17
RESULT 4
ABP52295 standard; peptide; 19 AA.
XX
AC      ABP52295;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
KW      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW      immune response; antiinflammatory; neuroprotective; proliferation;
KW      MHC class II protein inhibitor; demyelinating disease; inhibition;
KW      post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW      anti-tumour necrosis factor agent.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-US002071.
XX
PR      24-JAN-2001; 2001US-0263569P.
XX
PA      (HARD ) HARVARD COLLEGE.
XX
PI      Strominger JL, Fridkis-Hareli M;
XX
DR      WPI; 2002-608439/65.
XX
PT      New compositions comprising synthetic peptides in complex with a major
PT      histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT      demyelinating disease, e.g. multiple sclerosis, or post-viral
PT      encephalomyelitis.
XX
PS      Claim 28; Page 39; 54pp; English.
XX
CC      The present invention describes compositions (I) comprising a peptide
CC      with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC      residues. The complex of the peptide with a major histocompatibility
CC      complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC      immune response. (I) has antiinflammatory and neuroprotective activities,
CC      and can be used as a MHC class II protein inhibitor. The compositions
CC      comprising the peptides are useful for treating demyelinating diseases
CC      such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC      demyelinating condition, and a side effect of administering an anti-
CC      tumour necrosis factor agents. The peptide further inhibits proliferation
CC      of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC      ABP52305 represent peptides used in the exemplification of the present
CC      invention
XX
SQ      Sequence 19 AA;
Query Match      86.9%; Score 73; DB 5; Length 19;
Best Local Similarity 88.2%; Pred. No. 6.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      1 APEKAKFEAYKAAAPPA 17
      |||||:|||||
      |||||:|||||
AC      ABP52297
DB      1 APEKAKYEAYKAAAAA 17
RESULT 5
ABP52297 standard; peptide; 15 AA.
ID      ABP52297 standard; peptide; 15 AA.
```

```
XX
AC      ABP52297;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KW      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW      immune response; antiinflammatory; neuroprotective; proliferation;
KW      MHC class II protein inhibitor; demyelinating disease; inhibition;
KW      post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW      anti-tumour necrosis factor agent.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-US002071.
XX
PR      24-JAN-2001; 2001US-0263569P.
XX
PA      (HARD ) HARVARD COLLEGE.
XX
PI      Strominger JL, Fridkis-Hareli M;
XX
DR      WPI; 2002-608439/65.
XX
PT      New compositions comprising synthetic peptides in complex with a major
PT      histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT      demyelinating disease, e.g. multiple sclerosis, or post-viral
PT      encephalomyelitis.
XX
PS      Claim 28; Page 39; 54pp; English.
XX
CC      The present invention describes compositions (I) comprising a peptide
CC      with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC      residues. The complex of the peptide with a major histocompatibility
CC      complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC      immune response. (I) has antiinflammatory and neuroprotective activities,
CC      and can be used as a MHC class II protein inhibitor. The compositions
CC      comprising the peptides are useful for treating demyelinating diseases
CC      such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC      demyelinating condition, and a side effect of administering an anti-
CC      tumour necrosis factor agents. The peptide further inhibits proliferation
CC      of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC      ABP52305 represent peptides used in the exemplification of the present
CC      invention
XX
SQ      Sequence 15 AA;
Query Match      81.0%; Score 68; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00034;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      3 EKAKEAYKAAAPPA 17
      |||||:|||||
      |||||:|||||
DB      1 EKPKEAYKAAAPPA 15
RESULT 6
ABP52291 standard; peptide; 15 AA.
ID      ABP52291 standard; peptide; 15 AA.
XX
AC      ABP52291;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:85.
XX
```

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 77.4%; Score 65; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0011;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 EKAKFEAYKAAAPAA 17  
Db 1 EKPKYEAYKAAAPAA 15  
XX  
RESULT 7  
ABP52271  
ID ABP52271 standard; peptide; 15 AA.  
XX  
AC ABP52271;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 24-JAN-2002; 2002WO-US002071.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
DR WPI; 2002-608439/65.  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 73.8%; Score 62; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0033;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 EKAKFEAYKAAAPAA 17  
Db 1 EKAKYEAYKAAAPAAA 15  
XX  
RESULT 8  
ABP52298  
ID ABP52298 standard; peptide; 15 AA.  
XX  
AC ABP52298;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX

PF 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
XX Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 73.8%; Score 62; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0033;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 3 EKAKFEAYKAAAPAA 17  
DB 1 EKAKFEAYKAAAPAA 15  
RESULT 9  
ABP52304  
ID ABP52304 standard; peptide; 15 AA.  
XX  
XX ABP52304;  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:98.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200259143-A2.  
XX  
XX 01-AUG-2002.  
PD  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
PI

XX  
XX WPI; 2002-608439/65.  
XX  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
XX Claim 28; Page 39; 54pp; English.  
XX  
XX  
XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 73.8%; Score 62; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0033;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 3 EKAKFEAYKAAAPAA 17  
DB 1 EKAKFEAYKAAAPAA 15  
RESULT 10  
ABP52296  
ID ABP52296 standard; peptide; 17 AA.  
XX  
XX ABP52296;  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX HLA-DR2 molecule binding peptide SEQ ID NO:90.  
DE  
XX  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200259143-A2.  
XX  
XX 01-AUG-2002.  
PD  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
PT

XX Claim 28; Page 39; 54pp; English.

PS

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

CC

XX Sequence 17 AA;

XX

Query Match 73.8%; Score 62; DB 5; Length 17;

Best Local Similarity 86.7%; Pred. No. 0.0037;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKAKFEAYKAAAPAA 17

DB 1 EKAKFEAYKAAAPAA 15

RESULT 11

ABP52301

ID ABP52301 standard; peptide; 15 AA.

XX

AC ABP52301;

XX

DT 16-OCT-2002 (first entry)

DE

XX HLA-DR2 molecule binding peptide SEQ ID NO:95.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD ) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX

XX Sequence 15 AA;

XX

Query Match 72.6%; Score 61; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0048;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKAKFEAYKAAAPAA 17

DB 1 EKAKFEAYKAAAPAA 15

RESULT 12

ABP52299

ID ABP52299 standard; peptide; 15 AA.

XX

AC ABP52299;

XX

DT 16-OCT-2002 (first entry)

DE

XX HLA-DR2 molecule binding peptide SEQ ID NO:93.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD ) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present  
XX invention  
SQ Sequence 15 AA;  
Query Match 72.6%; Score 61; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0048;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKAKFEAYKAAAPA 17  
DB 1 EKPKVEAYKAAAPA 15  
RESULT 13  
ABP52290  
ID ABP52290 standard; peptide; 15 AA.  
XX  
AC ABP52290;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:84.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
PF 24-JAN-2001; 2001US-0263569P.  
XX  
PR 24-JAN-2001; 2001US-0263569P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
DR  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 70.2%; Score 59; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.01;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKAKFEAYKAAAPA 17  
DB 1 EAPKYEAYKAAAPA 15  
RESULT 14  
ABP52292  
ID ABP52292 standard; peptide; 15 AA.  
XX  
AC ABP52292;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
PI Strominger JL, Fridkis-Hareli M;  
XX  
XX WPI; 2002-608439/65.  
XX  
XX  
XX  
PT New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX  
XX  
CC The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
Query Match 70.2%; Score 59; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.01;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 EKAKFEAYKAAAPA 17  
DB 1 EAPKYEAYKAAAPA 15

```

RESULT 15
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
AC ABP52270;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15' AA;

Query Match 66.7%; Score 56; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.031;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKEAYKAAAPPA 17
   | | | | | | | | | |
Db 1 EAAKYEAYKAAAAAA 15

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Search completed: February 26, 2005, 23:48:25  
Job time : 87.9082 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:40:03 ; Search time 22.7245 Seconds  
(without alignments)  
55.844 Million cell updates/sec

Title: US-10-056-583A-97  
Perfect score: 84  
Sequence: 1 APEKAKFEAYKAAAPPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	53.6	145	US-09-640-211A-798	Sequence 798, App
2	45	53.6	212	US-09-902-540-16451	Sequence 16451, A
3	44	52.4	21	US-08-557-309B-58	Sequence 58, Appl
4	44	52.4	21	US-08-929-414-11	Sequence 11, Appl
5	44	52.4	21	US-08-834-306-56	Sequence 56, Appl
6	44	52.4	21	US-08-834-306-58	Sequence 58, Appl
7	44	52.4	21	US-08-993-674A-56	Sequence 56, Appl
8	44	52.4	21	US-08-993-674A-58	Sequence 58, Appl
9	44	52.4	21	US-09-256-976-56	Sequence 56, Appl
10	44	52.4	21	US-09-256-976-58	Sequence 58, Appl
11	44	52.4	262	US-08-403-379A-1	Sequence 1, Appl
12	44	52.4	262	US-08-929-414-1	Sequence 1, Appl
13	44	52.4	263	US-08-557-309B-51	Sequence 51, Appl
14	44	52.4	263	US-08-834-306-51	Sequence 51, Appl
15	44	52.4	263	US-08-993-674A-51	Sequence 51, Appl
16	44	52.4	263	US-09-256-976-51	Sequence 51, Appl
17	43	51.2	469	US-09-252-991A-27869	Sequence 27869, A
18	43	51.2	639	US-09-347-801-17	Sequence 17, Appl
19	43	51.2	639	US-09-854-731-17	Sequence 17, Appl
20	42	50.0	324	US-09-248-796A-17156	Sequence 17156, A
21	41	48.8	21	US-08-557-309B-61	Sequence 61, Appl
22	41	48.8	21	US-08-929-414-13	Sequence 13, Appl
23	41	48.8	21	US-08-834-306-60	Sequence 60, Appl
24	41	48.8	21	US-08-993-674A-60	Sequence 60, Appl
25	41	48.8	21	US-09-256-976-60	Sequence 60, Appl
26	41	48.8	245	US-08-486-099-104	Sequence 104, App
27	41	48.8	245	US-08-360-107A-114	Sequence 114, App

28	41	48.8	245	3	US-08-484-223B-104	Sequence 104, App
29	41	48.8	245	3	US-08-919-597-104	Sequence 104, App
30	41	48.8	245	3	US-08-475-668A-104	Sequence 104, App
31	41	48.8	245	3	US-08-485-551A-104	Sequence 104, App
32	41	48.8	245	3	US-08-471-913A-104	Sequence 104, App
33	41	48.8	245	3	US-08-485-264A-104	Sequence 104, App
34	41	48.8	245	3	US-08-474-349A-104	Sequence 104, App
35	41	48.8	245	4	US-08-470-896-104	Sequence 104, App
36	41	48.8	245	4	US-08-485-546A-104	Sequence 104, App
37	41	48.8	245	4	US-08-487-266A-104	Sequence 104, App
38	41	48.8	245	4	US-09-350-841A-1590	Sequence 1590, App
39	41	48.8	642	4	US-09-489-039A-12434	Sequence 12434, A
40	41	48.8	1020	4	US-09-538-092-911	Sequence 911, App
41	40.5	48.2	68	4	US-09-540-236-3324	Sequence 3324, App
42	40	47.6	21	1	US-08-403-379A-3	Sequence 3, Appl
43	40	47.6	21	2	US-08-557-309B-52	Sequence 52, Appl
44	40	47.6	21	2	US-08-557-309B-57	Sequence 57, Appl
45	40	47.6	21	2	US-08-557-309B-60	Sequence 60, Appl

## ALIGNMENTS

```
RESULT 1
US-09-640-211A-798
; Sequence 798, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Bucalypus grandis
; US-09-640-211A-798

Query Match          53.6%; Score 45; DB 4; Length 145;
Best Local Similarity 64.7%; Pred. No. 3.8;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 APEKAKFEAYKAAAPPA 17
Db      113 APIPASFSAPSAAPPA 129

RESULT 2
US-09-902-540-16451
; Sequence 16451, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16451
; LENGTH: 212
; TYPE: PRT
```

ORGANISM: Myxococcus xanthus  
US-09-902-540-16451

Query Match 53.6%; Score 45; DB 4; Length 212;  
Best Local Similarity 60.0%; Pred. No. 5.8;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 PEKAKFEAYKAAAP 16  
DB 134 PDQAPFDATLAAAA 148

## RESULT 3

US-08-557-309B-58

Sequence 58, Application US/08557309B  
Patent No. 5916572

## GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,309B

FILING DATE: 14-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-557-309B-58

Query Match 52.4%; Score 44; DB 2; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
DB 5 APAKAAAAAPAKAAAPA 21

## RESULT 4

US-08-929-414-11

Sequence 11, Application US/08929414  
Patent No. 5942403

## GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Haughton, Raymond

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION

TITLE OF INVENTION: OF T. CRUZI INFECTION

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,414

FILING DATE: 15-SEP-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.406C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-929-414-11

Query Match 52.4%; Score 44; DB 2; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
DB 5 APAKAAAAAPAKAAAPA 21

## RESULT 5

US-08-834-306-56

Sequence 56, Application US/08834306  
Patent No. 6054135

## GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,306

FILING DATE: 15-APR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-834-306-56

Query Match 52.4%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APEKAKFEAYKAAAPAA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPAA 21

## RESULT 6

US-08-834-306-58  
Sequence 58, Application US/08834306  
Patent No. 6054135  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,306  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-834-306-58

Query Match 52.4%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APEKAKFEAYKAAAPAA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPAA 21

RESULT 7  
US-08-993-674A-56  
Sequence 56, Application US/08993674A

Patent No. 6228372  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,674A  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-993-674A-56

Query Match 52.4%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APEKAKFEAYKAAAPAA 17  
||| |||||  
Db 5 APAKAAAPAKAAAPAA 21

## RESULT 8

US-08-993-674A-58  
Sequence 58, Application US/08993674A  
Patent No. 6228372  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,674A  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-993-674A-58

Query Match 52.4%; Score 44; DB 3; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAP 17  
|||  
Db 5 APAKAAAPAKAAAP 21

## RESULT 9

US-09-256-976-56  
Sequence 56, Application US/09256976  
Patent No. 6419933  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
FILE REFERENCE: 210121.422C3  
CURRENT APPLICATION NUMBER: US/09/256,976  
CURRENT FILING DATE: 1999-02-24  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 56  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Tce antigenic  
US-09-256-976-56:

Query Match 52.4%; Score 44; DB 4; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAP 17  
|||  
Db 5 APAKAAAPAKAAAP 21

## RESULT 10

US-09-256-976-58  
Sequence 58, Application US/09256976  
Patent No. 6419933  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Smith, John M.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
FILE REFERENCE: 210121.422C3  
CURRENT APPLICATION NUMBER: US/09/256,976  
CURRENT FILING DATE: 1999-02-24  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 58  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Tce  
US-09-256-976-58

Query Match 52.4%; Score 44; DB 4; Length 21;  
Best Local Similarity 64.7%; Pred. No. 0.65;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAP 17  
|||  
Db 5 APAKAAAPAKAAAP 21

## RESULT 11

US-08-403-379A-1  
Sequence 1, Application US/08403379A  
Patent No. 5756662  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
TITLE OF INVENTION: OF T. CRUZI INFECTION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,379A  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-379A-1

Query Match 52.4%; Score 44; DB 1; Length 262;  
Best Local Similarity 64.7%; Pred. No. 11;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17  
|||  
Db 141 APAKAAAPAKAAAPA 157

## RESULT 12

US-08-929-414-1  
; Sequence 1, Application US/08929414  
; Patent No. 5942403  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Haughton, Raymond  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION  
; TITLE OF INVENTION: OF T. CRUZI INFECTION  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/929,414  
; FILING DATE: 15-SEP-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.406C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 262 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-929-414-1

Query Match 52.4%; Score 44; DB 2; Length 262;  
Best Local Similarity 64.7%; Pred. No. 11;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17  
|||  
Db 141 APAKAAAPAKAAAPA 157

## RESULT 13

US-08-557-309B-51  
; Sequence 51, Application US/08557309B  
; Patent No. 5916572  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA

ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557,309B  
; FILING DATE: 14-NOV-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.422  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-557-309B-51

Query Match 52.4%; Score 44; DB 2; Length 263;  
Best Local Similarity 64.7%; Pred. No. 11;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAFAYKAAAPA 17  
|||  
Db 142 APAKAAAPAKAAAPA 158

## RESULT 14

US-08-834-306-51  
; Sequence 51, Application US/08834306  
; Patent No. 6054135  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,306  
; FILING DATE: 15-APR-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.422C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 263 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:

; TOPOLOGY: linear  
US-08-834-306-51

Query Match 52.4%; Score 44; DB 3; Length 263;  
Best Local Similarity 64.7%; Pred. No. 11;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
Db 142 APAKAAAAPAKAAAPA 158

RESULT 15  
US-08-993-674A-51

; Sequence 51, Application US/08993674A  
; Patent No. 6228372

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skelky, Yasir A.W.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Smith, John M.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/993,674A

; FILING DATE: 18-DEC-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.422C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 263 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-993-674A-51

Query Match 52.4%; Score 44; DB 3; Length 263;  
Best Local Similarity 64.7%; Pred. No. 11;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
Db 142 APAKAAAAPAKAAAPA 158

Search completed: February 26, 2005, 23:59:31  
Job time : 23.7245 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 26, 2005, 23:45:03 ; Search time 60.7143 Seconds  
(without alignments)  
91.852 Million cell updates/sec

Title: US-10-056-583A-97  
Perfect score: 84  
Sequence: 1 APEKAKFEAYKAAAPA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	17	US-10-056-583-97	Sequence 97, Appl
2	80	95.2	17	US-10-056-583-96	Sequence 96, Appl
3	73	86.9	17	US-10-056-583-88	Sequence 88, Appl
4	73	86.9	19	US-10-056-583-89	Sequence 89, Appl
5	68	81.0	15	US-10-056-583-91	Sequence 91, Appl
6	65	77.4	15	US-10-056-583-85	Sequence 85, Appl
7	62	73.8	15	US-10-056-583-65	Sequence 65, Appl
8	62	73.8	15	US-10-056-583-98	Sequence 98, Appl
9	62	73.8	17	US-10-056-583-90	Sequence 90, Appl
10	61	72.6	15	US-10-056-583-93	Sequence 93, Appl
11	61	72.6	15	US-10-056-583-95	Sequence 95, Appl
12	59	70.2	15	US-10-056-583-84	Sequence 84, Appl
13	59	70.2	15	US-10-056-583-86	Sequence 86, Appl

14	56	66.7	15	14	US-10-056-583-64	Sequence 64, Appl
15	56	66.7	15	14	US-10-056-583-92	Sequence 92, Appl
16	55	65.5	15	14	US-10-056-583-94	Sequence 94, Appl
17	55	65.5	15	14	US-10-056-583-99	Sequence 99, Appl
18	52	61.9	15	14	US-10-056-583-57	Sequence 57, Appl
19	51	60.7	15	14	US-10-056-583-66	Sequence 66, Appl
20	50	59.5	15	14	US-10-056-583-51	Sequence 51, Appl
21	50	59.5	15	14	US-10-056-583-53	Sequence 53, Appl
22	49	58.3	15	14	US-10-056-583-83	Sequence 83, Appl
23	47	56.0	15	14	US-10-056-583-33	Sequence 33, Appl
24	47	56.0	15	14	US-10-056-583-45	Sequence 45, Appl
25	47	56.0	15	14	US-10-056-583-47	Sequence 47, Appl
26	46	54.8	15	14	US-10-056-583-38	Sequence 38, Appl
27	46	54.8	15	14	US-10-056-583-55	Sequence 55, Appl
28	46	54.8	15	14	US-10-056-583-56	Sequence 56, Appl
29	46	54.8	15	14	US-10-056-583-63	Sequence 63, Appl
30	46	54.8	15	14	US-10-094-749-3117	Sequence 3117, Ap
31	46	54.8	15	14	US-10-408-765A-2514	Sequence 2514, Ap
32	45	53.6	15	14	US-10-056-583-30	Sequence 30, Appl
33	45	53.6	15	14	US-10-056-583-58	Sequence 58, Appl
34	45	53.6	15	14	US-10-056-583-61	Sequence 61, Appl
35	45	53.6	15	14	US-10-056-583-87	Sequence 87, Appl
36	45	53.6	203	15	US-10-369-493-19276	Sequence 19276, A
37	45	53.6	265	15	US-10-424-599-180279	Sequence 180279, A
38	45	53.6	265	15	US-10-425-114-54748	Sequence 54748, A
39	43	51.2	15	14	US-10-056-583-59	Sequence 59, Appl
40	43	51.2	180	15	US-10-424-599-266399	Sequence 266399, A
41	43	51.2	267	16	US-10-437-963-134556	Sequence 134556, A
42	43	51.2	386	16	US-10-437-963-194029	Sequence 194029, A
43	43	51.2	404	16	US-10-437-963-134562	Sequence 134562, A
44	43	51.2	421	15	US-10-282-122A-56483	Sequence 56483, A
45	43	51.2	465	15	US-10-282-122A-66168	Sequence 66168, A

## ALIGNMENTS

RESULT 1  
US-10-056-583-97  
; Sequence 97, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
; US-10-056-583-97

Query Match 100.0%; Score 84; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPA 17  
Db 1 APEKAKFEAYKAAAPA 17

RESULT 2  
US-10-056-583-96

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; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
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Query Match          95.2%; Score 80; DB 14; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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        |||||:|||||
Db      1 APEKAKFEAYKAAAPAA 17
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## RESULT 3

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US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

```
Query Match          86.9%; Score 73; DB 14; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 APEKAKFEAYKAAAPAA 17
        |||||:|||||
Db      1 APEKAKFEAYKAAAPAA 17
```

## RESULT 4

```
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match          86.9%; Score 73; DB 14; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 APEKAKFEAYKAAAPAA 17
        |||||:|||||
Db      1 APEKAKFEAYKAAAPAA 17
```

## RESULT 5

```
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
```

```
Query Match          81.0%; Score 68; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 EKAKFEAYKAAAPAA 17
        |||||:|||||
Db      1 EKPKFEAYKAAAPAA 15
```

## RESULT 6

```
US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match      77.4%; Score 65; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00048;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EKAKEAYKAAAPAA 17
      |||:|||||
Db      1 EKPKEAYKAAAPAA 15

RESULT 7
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

Query Match      73.8%; Score 62; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EKAKEAYKAAAPAA 17
      |||:|||||
Db      1 EKAKEAYKAAAPAA 15

RESULT 8
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
```

```
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98

Query Match      73.8%; Score 62; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 EKAKEAYKAAAPAA 17
      |||:|||||
Db      1 EAPKEAYKAAAPAA 15

RESULT 9
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

Query Match      73.8%; Score 62; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EKAKEAYKAAAPAA 17
      |||:|||||
Db      1 EKAKEAYKAAAPAA 15

RESULT 10
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
```

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-93

Query Match 72.6%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EKPKEAYKAAAPAA 15

RESULT 11  
US-10-056-583-95

; Sequence 95, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-95

Query Match 72.6%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0022;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EKAKFEAYKAAAPAA 15

RESULT 12  
US-10-056-583-84

; Sequence 84, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-84

Query Match 70.2%; Score 59; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0048;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 13  
US-10-056-583-86

; Sequence 86, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-86

Query Match 70.2%; Score 59; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0048;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 14  
US-10-056-583-64

; Sequence 64, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-64

Query Match 66.7%; Score 56; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.015;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPAA 17  
| | | | | | | | | | | | | | | | |  
Db 1 EAKYEAYKAAAPAA 15

## RESULT 15

US-10-056-583-92

; Sequence 92, Application US/10056583  
; Publication No. US20030064915A1

## ; GENERAL INFORMATION:

; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/10/056,583

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 92

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.

US-10-056-583-92

Query Match 66.7%; Score 56; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.015;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKFEAYKAAAPA 17  
|||||

Db 1 EKAKFEAYKAAAPA 15

Search completed: February 27, 2005, 00:05:24  
Job time : 61.7143 secs

**This Page Blank (uspto)**



A:Map position: circular chromosome  
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 54.8%; Score 46; DB 2; Length 179;  
Best Local Similarity 64.7%; Pred. No. 3.1;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
|||:|||||  
Db 135 ABEKARLEAEKVAAAQA 151

## RESULT 3

hypothetical protein CC0674 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: G87332

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87332  
A:Molecule type: preliminary  
A:Status: preliminary  
A:Residues: 1-389 <STO>  
A:Cross-references: UNIPROT:Q9AAC6; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:G  
C:Genetics:  
A:Gene: CC0674

Query Match 53.6%; Score 45; DB 2; Length 389;  
Best Local Similarity 58.8%; Pred. No. 9.6;  
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
|||:|||||  
Db 63 ADGKTSVETFEKAAAPA 79

## RESULT 4

diHydroliipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Brucella melitensis (S  
AH3269

C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: AH3269

R;DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
. ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens  
A:Reference number: AD3252; PMID:11756688

A:Accession: AH3269  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-408 <KUR>  
A:Cross-references: UNIPROT:Q9L6H8; GB:AE008917; PIDN:AAL51323.1; PID:g17982020; GSPDB:G  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI0141

A:Map position: I  
C:Superfamily: diHydroliipoamide acetyltransferase; 1lpoyl/biotin-binding homology  
C:Keywords: acyltransferase; coenzyme A

Query Match 53.6%; Score 45; DB 2; Length 408;  
Best Local Similarity 64.7%; Pred. No. 10;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
|||:|||||  
Db 86 APAQKKEAKPAAAPA 102

RESULT 5  
S40015

phd protein - phage P1

C:Species: phage P1  
C:Date: 25-Dec-1994 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S40015; S38553

R;Lehnher, H.; Maguin, E.; Jafri, S.; Yarmolinsky, M.B.

J. Mol. Biol. 233, 414-428, 1993

A:Title: Plasmid addition genes of bacteriophage P1: doc, which causes cell death on cu  
A:Reference number: S40015; MUID:94016561; PMID:8411153

A:Accession: S40015  
A:Molecule type: DNA  
A:Residues: 1-73 <LEH>  
A:Cross-references: UNIPROT:Q06253; GB:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645  
R;Schmidt, C.; Lehnher, H.; Guidolin, A.; Arber, W.  
submitted to the EMBL Data Library, November 1992  
A:Description: Additional late promoter sequences of bacteriophage P1.  
A:Reference number: S38553  
A:Accession: S38553  
A:Molecule type: DNA  
A:Residues: 1-73 <SCH>  
A:Cross-references: EMBL:M95666; NID:g463276; PIDN:AAA16932.1; PID:g215645

Query Match 52.4%; Score 44; DB 2; Length 73;  
Best Local Similarity 71.4%; Pred. No. 2.7;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 KAKFEAYKAAAPA 17  
|||:|||||  
Db 41 KATFEAYKKAALDA 54

## RESULT 6

repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)

C:Species: Trypanosoma cruzi

C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
C:Accession: G60110

R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E  
Infect. Immun. 57, 1959-1967, 1989

A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.  
A:Reference number: A60110; MUID:89277508; PMID:2659529

A:Accession: G60110  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-97 <HOF>  
A:Cross-references: UNIPROT:Q7M3W1  
C:Superfamily: varicella-zoster virus gene 22 protein  
C:Keywords: tandem repeat  
F,1-85/Region: 7-residue repeats

Query Match 52.4%; Score 44; DB 2; Length 97;  
Best Local Similarity 64.7%; Pred. No. 3.6;  
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17  
|||:|||||  
Db 2 APKAAAPAKAAAPA 18

## RESULT 7

tolA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: JY0057; B64810

R;Levengood, S.K.; Webster, R.E.

J. Bacteriol. 171, 6600-6609, 1989

A:Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ  
A:Reference number: JY0057; MUID:90078104; PMID:2687247  
A:Accession: JY0057  
A:Molecule type: DNA  
A:Residues: 1-421 <LEV>

A:Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019  
A:Experimental source: strain JM105  
A:Note: the authors translated the initiation codon GTG for residue 1 as Val  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of *Escherichia coli* K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: B64810  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-421 <BLAT>  
A:Cross-references: GB:AE00177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;  
A:Experimental source: strain K-12, substrain MG1655  
C:Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t  
C:Genetics:  
A:Gene: tolA  
A:Map position: 17 min  
A:Start codon: GTG  
C:Keywords: nucleotide binding; P-loop; transmembrane protein  
F:14-34/Domain: transmembrane #status predicted <MSS>  
F:78-301/Domain: helical #status predicted <HSR>  
F:355-362/Region: nucleotide-binding motif A (P-loop)

Query Match 51.2%; Score 43; DB 2; Length 421;  
Best Local Similarity 73.3%; Pred. No. 22;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPA 15  
|:|||||:|  
Db 215 AA EKAKAEAEKKA 229

RESULT 8  
D83598  
probable zinc proteinase PA0372 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: D83598  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Ladbeg, K.; Llm,  
.J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: D83598  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-465 <STO>  
A:Cross-references: UNIPROT:Q916C2; GB:AE004475; GB:AE004091; NID:g9946221; PIDN:AAG0376  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0372

Query Match 51.2%; Score 43; DB 2; Length 465;  
Best Local Similarity 56.2%; Pred. No. 25;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKFEAYKAAAPA 17  
|:|||||:|  
Db 172 PNALAFERFKAAAYPA 187

RESULT 9  
T02784  
calcium-dependent protein kinase (BC 2.7.1.1) - maize (strain W64A)  
C:Species: *Zea mays* (maize)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T02784  
R:Murillo, I.; Jaack, E.; Cordero, M.; San Segundo, B.  
submitted to the EMBL Data Library, July 1998  
A:Description: A calcium-dependent protein kinase possibly involved in pathogen defense  
sis-related Prms gene.

A:Reference number: Z14736  
A:Accession: T02784  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-639 <MUR>  
A:Cross-references: UNIPROT:O82107; EMBL:AJ007366; PIDN:CAA07481.1  
A:Experimental source: strain W64A; seed  
C:Function:  
A:Description: probably involved in pathogen defense in maize plants  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F:151-411/Domain: protein kinase homology <KIN>  
F:159-167/Region: protein kinase ATP-binding motif  
F:454-486/Domain: calmodulin repeat homology <EF1>  
F:490-522/Domain: calmodulin repeat homology <EF2>  
F:526-558/Domain: calmodulin repeat homology <EF3>  
F:560-592/Domain: calmodulin repeat homology <EF4>  
F:182/Active site: Lys #status predicted

Query Match 51.2%; Score 43; DB 1; Length 639;  
Best Local Similarity 52.9%; Pred. No. 34;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKAAAPA 17  
|:|||||:|  
Db 68 APEPVKIAVHSEPA 84

RESULT 10  
S77930  
exoskeletal protein HACP202A - American lobster (fragment)  
C:Species: *Homarus americanus* (American lobster)  
C>Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77930  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, *Homa*  
A:Reference number: S77925  
A:Accession: S77930  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M496

Query Match 50.6%; Score 42.5; DB 2; Length 189;  
Best Local Similarity 61.1%; Pred. No. 12;  
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAKFEAYKAAAPA 17  
|:|||||:|  
Db 9 AA EKARFFQAFKAEAAA 26

RESULT 11  
S77935  
exoskeletal protein HACP202B - American lobster (fragment)  
C:Species: *Homarus americanus* (American lobster)  
C>Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77935  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, *Homa*  
A:Reference number: S77925  
A:Accession: S77935  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M495

Query Match 50.6%; Score 42.5; DB 2; Length 189;  
Best Local Similarity 61.1%; Pred. No. 12;  
Matches 11; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 APEKAKFEAYKAAAP 17  
| | | | : : : : | | | |  
Db 9 AAEKARFEQAFKAAEAAA 26

## RESULT 12

T23177  
hypothetical protein K01D12.7 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T23177; T23188  
R/Dobson, R.  
submitted to the EMBL Data Library, June 1996  
A/Reference number: Z19703  
A/Accession: T23177  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-84 <WIL>  
A/Cross-references: UNIPROT:Q27223; UNIPROT:Q95QD3; EMBL:Z75543; PIDN:CAA99866.1; GSPDB:  
A/Experimental source: clone K01D12  
A/Accession: T23188  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-84 <WIL>  
A/Cross-references: EMBL:Z75543; PIDN:CAA99878.1; GSPDB:GN00023; CESP:K01D12.15  
A/Experimental source: clone K01D12  
C/Genetics:  
A/Gene: CESP:K01D12.7; CESP:K01D12.15  
A/Map position: 5

Query Match 50.0%; Score 42; DB 2; Length 84;  
Best Local Similarity 62.5%; Pred. No. 6.7;  
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 PEKAKFEAYKAAAP 17  
| | | | : : : : | | | |  
Db 34 PPKASASATKAAAP 49

## RESULT 13

JC2184  
transcription factor Brn-3R - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 16-Aug-2004  
C/Accession: JC2184; S41455  
R/Jehn, B.; Chicaiza, G.; Martin, F.; Jaggi, R.  
Biochem. Biophys. Res. Commun. 200, 156-162, 1994  
A/Title: Isolation of three novel POU-domain containing cDNA clones from lactating mouse  
A/Reference number: JC2182; MUID:94220079; PMID:8166682  
A/Accession: JC2184  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-88 <JEH>  
A/Cross-references: UNIPROT:Q62091; EMBL:Z29629  
A/Experimental source: mammary gland  
R/Jehn, B.; Chicaiza, G.; Martin, F.; Jaggi, R.  
submitted to the EMBL Data Library, January 1994  
A/Description: Isolation of three novel POU-domain containing cDNA clones from lactating  
A/Reference number: S41454  
A/Accession: S41455  
A/Molecule type: mRNA  
A/Residues: 1-45, 'F', 47-88 <JE2>  
A/Cross-references: EMBL:Z29629; NID:G452415; PIDN:CAA82736.1; PID:G452416  
C/Superfamily: homeobox homology; POU domain homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/1-33/Domain: POU domain homology (fragment) <POU>  
F/49-88/Domain: homeobox homology (fragment) <HOX>

Query Match 50.0%; Score 42; DB 2; Length 88;  
Best Local Similarity 75.0%; Pred. No. 7;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKFEAYKA 12

Db 59 APEKASLEAYFA 70  
| | | | : : : : | | | |

## RESULT 14

AH2752  
dihydrolipoamide acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, D  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AH2752  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, B.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AH2752  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-405 <KUR>  
A/Cross-references: UNIPROT:Q8UFG5; GB:AE008668; PIDN:AAL42438.1; PID:g17739851; GSPDB:C  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: aceF  
A/Map position: circular chromosome

Query Match 50.0%; Score 42; DB 2; Length 405;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAKFEAYKAAAP 16  
| | | | : : : : | | | |  
Db 56 PEAAKAEAPKEEAP 70

## RESULT 15

F97533  
dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (e2) [imp  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97533  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: F97533  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-457 <KUR>  
A/Cross-references: UNIPROT:Q8UFG5; GB:AE007869; PIDN:AAK87223.1; PID:g15156505; GSPDB:C  
C/Genetics:  
A/Gene: AGR\_C\_2641  
A/Map position: circular chromosome  
C/Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 50.0%; Score 42; DB 2; Length 457;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAKFEAYKAAAP 16  
| | | | : : : : | | | |  
Db 108 PEAAKAEAPKEEAP 122

Search completed: February 26, 2005, 23:57:18  
Job time : 16.0918 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2005, 23:07:23 ; Search time 73.898 Seconds  
(without alignments)  
117.802 Million cell updates/sec

Title: US-10-056-583A-97  
Perfect score: 84  
Sequence: 1 APEKAKEAYKAAAPPA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	60.7	574	2 Q8SXM8	Q8sxm8 drosophila
2	51	60.7	607	2 Q9W327	Q9w327 drosophila
3	46	54.8	179	1 RL19_AGRT5	Q9ubz5 agrobacteri
4	46	54.8	570	2 Q96M46	Q96m46 homo sapien
5	45	53.6	183	2 Q81W24	Q81w24 bacillus an
6	45	53.6	244	2 Q8JHA3	Q8jha3 gallus gall
7	45	53.6	389	2 Q9AAC8	Q9aac8 caulobacter
8	45	53.6	390	2 Q85598	Q85598 brucella ab
9	45	53.6	408	2 Q8FYF8	Q8fyf8 brucella su
10	45	53.6	408	2 Q916H8	Q916h8 brucella me
11	45	53.6	607	2 Q8BGF8	Q8bgf8 xanthomonas
12	45	53.6	781	2 Q65JG3	Q65jg3 bacillus li
13	45	53.6	1340	2 Q69YQ8	Q69yq8 homo sapien
14	45	53.6	1614	2 Q69YQ9	Q69yq9 homo sapien
15	44.5	53.0	427	2 Q98EL9	Q98el9 rhizobium l
16	44	52.4	73	1 PHD_BPPI	Q06253 bacterioph
17	44	52.4	73	2 Q79A04	Q79a04 escherichia
18	44	52.4	87	2 Q8TUG9	Q8tjg9 methanosarc
19	44	52.4	97	2 Q7M3W1	Q7m3w1 trypanosoma
20	44	52.4	272	2 Q8P7P0	Q8p7p0 xanthomonas
21	44	52.4	2034	2 Q872S0	Q872s0 neurospora
22	43.5	51.8	306	2 Q7XJ35	Q7xj35 medicago tr
23	43	51.2	153	2 Q7XVT5	Q7xvt5 oryza sativ
24	43	51.2	163	2 Q6RS84	Q6jrs4 equus caball
25	43	51.2	174	2 Q73FU2	Q73fj2 bacillus ce
26	43	51.2	177	1 RL19_RHIME	Q92139 rhizobium m
27	43	51.2	181	1 RL19_RHIL0	P58168 rhizobium l
28	43	51.2	190	2 Q6AH83	Q6ah83 leifsonia x
29	43	51.2	238	2 Q62WL2	Q62wl2 bacillus li
30	43	51.2	240	2 Q65L73	Q65l73 bacillus li
31	43	51.2	404	2 Q7F9Q4	Q7f9q4 oryza sativ

32	43	51.2	413	2 Q83SA1	Q83sa1 shigella fl
33	43	51.2	421	1 TOLA_ECOLI	P19934 escherichia
34	43	51.2	421	2 Q8FJT1	Q8fjct1 escherichia
35	43	51.2	465	2 Q916C2	Q916c2 pseudomonas
36	43	51.2	593	2 Q6AQK4	Q6aqk4 desulfotale
37	43	51.2	639	2 Q82107	Q82107 zea mays (m
38	43	51.2	707	2 Q64CP3	Q64cp3 uncultured
39	43	51.2	1924	2 Q7R5U9	Q7rsu9 giardia lam
40	42.5	50.6	189	2 Q7M495	Q7m495 homarus ame
41	42.5	50.6	189	2 Q7M496	Q7m496 homarus ame
42	42.5	50.6	300	2 Q729M4	Q729m4 desulfovibr
43	42	50.0	88	2 Q62091	Q62091 mus musculu
44	42	50.0	151	2 Q95Z67	Q95z67 ostertagia
45	42	50.0	250	2 Q7NW09	Q7nw09 chromobacte

ALIGNMENTS

RESULT 1  
Q8SXM8 PRELIMINARY; PRT; 574 AA.  
ID Q8SXM8; AC Q8SXM8; DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE LD23509P (CG12141-PA).  
GN Name=AaCs-lys; ORFNames=CG12141;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkely;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.,  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., Mcleod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*";  
RL Science 287:2185-2195 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.F.,  
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
DR EMBL; AY089547; AAL90285.1; -.  
DR EMBL; AE003447; AAN09255.1; -.  
DR HSSP; P13030; IBBW.  
DR FlyBase; FBgn0027084; Aats-lys.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0004615; F:aspartate-tRNA ligase activity; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0006422; P:aspartyl-tRNA aminoacylation; IEA.  
DR GO; GO:0006430; P:lysyl-tRNA aminoacylation; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR InterPro; IPR008994; Nucleic acid\_OB.  
DR InterPro; IPR004364; tRNA-synt\_2.  
DR InterPro; IPR002312; tRNA-synt asp.  
DR InterPro; IPR002313; tRNA-synt\_lys\_2.  
DR InterPro; IPR004365; tRNA anti.  
DR InterPro; IPR006195; tRNA\_ligase\_II.

```

DR Pfam; PF00152; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHLVS.
DR TIGRFAMs; TIGR00499; lys_bact; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; ligase; Protein biosynthesis.
SQ SEQUENCE 574 AA; 64660 MW; 861DAEA9C53E0DBE CRC64;

Query Match 60.7%; Score 51; DB 2; Length 574;
Best Local Similarity 70.6%; Pred. No. 6.8;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps

QY 1 APEKAKFEAYKAAAPPA 17
|:|:|:|:|:|:|:|:|:|
Db 19 AEQAKAEKAEKAAAPPA 35

RESULT 2
Q9W327 PRELIMINARY; PRT; 607 AA.
ID Q9W327;
AC Q9W327;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG12141-PB.
GN ORFNames=CG12141;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernama B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M.W., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtksa R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein D., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
DR EMBL; AE003447; AAF46510.2; -.
DR HSSP; P13030; 1BBW.
DR FlyBase; FBgn0027084; Aats-lys.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004815; F:aspartate-tRNA ligase activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004824; F:lysine-tRNA ligase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006422; F:aspartyl-tRNA aminoacylation; IEA.
DR GO; GO:0006430; F:lysyl-tRNA aminoacylation; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004364; tRNA-synt_2.
DR InterPro; IPR002312; tRNA-synt_asp.
DR InterPro; IPR002313; tRNA-synt_lys_2.
DR InterPro; IPR004365; tRNA-anti.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF00152; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA-anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHLYS.
DR TIGRFAMs; TIGR00499; lys_bact; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; ligase; Protein biosynthesis.
SQ SEQUENCE 607 AA; 68503 MW; 771CE9870963D81B CRC64;

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Query Match 60.7%; Score 51; DB 2; Length 607;
Best Local Similarity 70.6%; Pred. No. 7.2;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 APEKAFBAYKAAAPA 17
|:|:|:|:|:|:|
Db 52 AEQAKKEKAKAAAPA 68

RESULT 3
RL19 AGRT5
ID RL19 AGRT5 STANDARD; PRT; 179 AA.
AC Q8UBZ5;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rpL5; OrderedLocustNames=Atu2703, AGR C 4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kiteajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Guorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L19 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE009216; AAL43684.1; -.
DR EMBL; AE008183; AAK88423.1; -.
DR PIR; AP2908; AP2908.
DR PIR; F97683; F97683.
DR HAMAP; MF_00402; -.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR PRODOM; PD002979; Ribosomal_L19; 1.
DR TIGRFAMs; TIGR01024; rPL5_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

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Query Match 54.8%; Score 46; DB 1; Length 179;  
 Best Local Similarity 64.7%; Pred. No. 15;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAEAYKAAAP 17  
 |||:|||||  
 Db 135 ABEKARLEAKVAAQA 151

## RESULT 4

Q96M46 PRELIMINARY; PRT; 570 AA.

AC Q96M46: PRELIMINARY; PRT; 570 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ32830.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
 Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,  
 Ono Y., Takiguchi S., Watanabe S., Yosida M., Houchi T., Kusano J.,  
 Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
 Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 Yoshiyama Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 Hishigaki H., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,  
 Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,  
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa R.,  
 Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,  
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 DR EMBL; AK057392; BAB71466.1; -.  
 DR InterPro; IPR008938; ARM.  
 SQ SEQUENCE 570 AA; 65769 MW; 65BEB6F244FC7E2 CRC64;

Query Match 54.8%; Score 46; DB 2; Length 570;  
 Best Local Similarity 61.5%; Pred. No. 46;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PEKAEAYKAAAP 14  
 |||:|||||  
 Db 194 PEKVYEAAYRTIA 206

RESULT 5  
 Q81W24 PRELIMINARY; PRT; 183 AA.

AC Q81W24; Q61526; Q6KYS0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=BA0013, BAS0016, GBA00013;  
 OS Bacillus anthracis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Ames / isolate Porton;  
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
 RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,  
 Nelson K.E., Tettein H., Fouts D.E., Eisen J.A., Gill S.R.,  
 Holtzaple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,  
 Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
 DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Niernan W.C.,  
 Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,  
 Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
 RA "The genome sequence of Bacillus anthracis Ames and comparison to  
 closely related bacteria.";  
 RT Nature 423:81-86(2003).  
 RL [2]  
 RN SEQUENCE FROM N.A.

RP STRAIN=Ames / isolate 0581;  
 RC Ravel J., Rasbo D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
 Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
 Fraser C.M.;  
 RA "Bacillus anthracis comparative genomics.";  
 RT Submitted (May-2004) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RN SEQUENCE FROM N.A.

RP STRAIN=Sterne;  
 RC Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 Richardson P., Rubin E., Tice H.;  
 RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AE017024; AAP24070.1; -.  
 DR EMBL; AE017334; AAT29093.1; -.  
 DR EMBL; AE017225; AAT52355.1; -.  
 DR TIGR; BA0013; -.  
 DR TIGR; GBA0013; -.  
 DR InterPro; IPR009058; Wing\_hlx DNA bnd.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 183 AA; 20653 MW; 3BD4AC2C8D658752 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 183;  
 Best Local Similarity 62.5%; Pred. No. 23;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAEAYKAAAP 16  
 |||:|||||  
 Db 116 APKVKKEAVKKEAP 131

## RESULT 6

Q8JHA3 PRELIMINARY; PRT; 244 AA.

AC Q8JHA3: PRELIMINARY; PRT; 244 AA.  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Class IV POU-domain transcription factor Brn-3.2 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Huverstuhl J., Broers D., Bodmer D., Mullen L., Gleich O., Strutz J.,
RA Ryan A.F.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF526419; AAM89245.1; -.
DR HSSP; P14859; ICQT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR01356; Homeobox.
DR InterPro; IPR010982; lambda_like_DNA.
DR InterPro; IPR00327; POU.
DR Pfam; PF00157; Pou; 1.
DR PRINTS; PRD0028; POUDOMAIN.
DR ProDom; PD00010; Homeobox; 1.
DR ProDom; PD000583; POU; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 244 AA; 26554 MW; 59D36AB50611BD9D CRC64;

Query Match 53.6%; Score 45; DB 2; Length 244;
Best Local Similarity 58.8%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17
Db 219 APEKRSLEAYFALQPPA 235

RESULT 7
O9AAC8 : PRELIMINARY; PRT; 389 AA.
ID O9AAC8 :
AC O9AAC8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein CC0674.
GN OrderedLocusNames=CC0674;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eissen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005743; AAK22659.1; -.
DR PIR; G87332; G87332.
DR TIGR; CC0674; -.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000897; SRP54.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 389 AA; 40769 MW; C6DD05B8CE8D150E CRC64;

Query Match 53.6%; Score 45; DB 2; Length 389;
Best Local Similarity 58.8%; Pred. No. 47;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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OY 1 APEKAKFEAYKAAAPA 17
Db 63 ADGKTSVETFKAAAPA 79

RESULT 8
O85598 : PRELIMINARY; PRT; 390 AA.
ID O85598 :
AC O85598;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Dihydrolipoamide succinyl transferase.
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S19;
RA Boschiroli L., Cravero S., Rosetti O.L.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
DR EMBL; AF070932; AAC23605.1; -.
DR HSSP; P07016; IC4T.
DR GO; GO:045252; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. .; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR01078; 2oxoacid_dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR011053; Hybrid_motif.
DR InterPro; IPR006255; SUCB.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF02817; E3_binding; 1.
DR ProDom; PD001115; 2oxoacid_dh; 1.
DR TIGRFAMs; TIGR01347; sucB; 1.
DR ACyltransferase; Lipoyl; Transferase.
KW ACyltransferase; Lipoyl; 41004 MW; 5A0AAD87569F5C2 CRC64;
SQ SEQUENCE 390 AA; 41004 MW; 5A0AAD87569F5C2 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 390;
Best Local Similarity 64.7%; Pred. No. 47;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 APEKAKFEAYKAAAPA 17
Db 71 APAQKEAKPAAAPA 87

RESULT 9
O8FYF8 : PRELIMINARY; PRT; 408 AA.
ID O8FYF8 :
AC O8FYF8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide
DE succinyltransferase (EC 2.3.1.61).
GN Name=sucB; OrderedLocusNames=BR1922;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / B1ovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
```

RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,  
 RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,  
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,  
 RA Fraser C.M.;  
 RT "The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
 DR EMBL; AE014482; AAN30814.1; -.  
 DR HSSP; P07016; 1C4T.  
 DR TIGR; BR1922; -.  
 DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
 DR GO; GO:0008415; F:acyltransferase activity; IEA.  
 DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
 DR InterPro; IPR001078; 2Oxoacid\_dh.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR004167; E3\_binding.  
 DR InterPro; IPR011053; Hybrid\_motif.  
 DR InterPro; IPR003016; Lipoyl\_BS.  
 DR InterPro; IPR006255; SucB.  
 DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF02817; E3\_binding; 1.  
 DR ProDom; PD001115; 2Oxoacid\_dh; 1.  
 DR TIGRFAMs; TIGR01347; sucB; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 DR Acyltransferase; Complete proteome; Lipoyl; Transferase.  
 KW Acyltransferase; Complete proteome; Lipoyl; Transferase.  
 SQ SEQUENCE 408 AA; 42839 MW; 7EC80A61800ACC64 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 408;  
 Best Local Similarity 64.7%; Pred. No. 49;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAKFEAYKAAAPA 17  
 ||:|||||  
 Db 86 APAQKKEAKPAAAPA 102

## RESULT 10

Q9L6H8 PRELIMINARY; PRT; 408 AA.  
 ID Q9L6H8  
 AC Q9L6H8; Q7CNV5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE  
 DE DEHYDROGENASE COMPLEX (EC 2.3.1.61).  
 GN Name=sucB; OrderedlocusNames=BMEI0141;  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M;  
 RX MEDLINE=21437665; PubMed=11553602;  
 DOI=10.1128/IAI.69.10.6537-6540.2001;  
 RA Zygmunt M.S., Diaz M.A., Teixeira-Gomes A.P., Cloeckaert A.;  
 RT "Cloning, nucleotide sequence, and expression of the Brucella  
 RT melitensis sucB gene coding for an immunogenic dihydrolipoamide  
 RT succinyltransferase homologous protein.";  
 RL Infect. Immun. 69:6537-6540(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;

RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyriades N.C., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
 DR EMBL; AF235020; AAF43701.1; -.  
 DR EMBL; AE009457; AAL51323.1; -.  
 DR PIR; AH3269; AH3269.  
 DR HSSP; P07016; 1C4T.  
 DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.  
 DR GO; GO:0008415; F:acyltransferase activity; IEA.  
 DR GO; GO:0004149; F:dihydrolipoyllysine-residue succinyltransfe. . .; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.  
 DR InterPro; IPR001078; 2Oxoacid\_dh.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR004167; E3\_binding.  
 DR InterPro; IPR011053; Hybrid\_motif.  
 DR InterPro; IPR003016; Lipoyl\_BS.  
 DR InterPro; IPR006255; SucB.  
 DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF02817; E3\_binding; 1.  
 DR ProDom; PD001115; 2Oxoacid\_dh; 1.  
 DR TIGRFAMs; TIGR01347; sucB; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 DR Acyltransferase; Complete proteome; Lipoyl; Transferase.  
 KW Acyltransferase; Complete proteome; Lipoyl; Transferase.  
 SQ SEQUENCE 408 AA; 42911 MW; 16E763942B097CA7 CRC64;

Query Match 53.6%; Score 45; DB 2; Length 408;  
 Best Local Similarity 64.7%; Pred. No. 49;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APEKAKFEAYKAAAPA 17  
 ||:|||||  
 Db 86 APAQKKEAKPAAAPA 102

## RESULT 11

Q8PGF8 PRELIMINARY; PRT; 607 AA.  
 ID Q8PGF8  
 AC Q8PGF8;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Dihydrolipoamide dehydrogenase.  
 GN Name=lpdA; OrderedlocusNames=XAC3659;  
 OS Xanthomonas axonopodis (pv. citri).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=92829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Cannavan F., Cardozo U., Chamberg F., Ciapina L.P.,  
 RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,  
 RA Faria J.B., Ferreira A.U.S., Ferreira R.C.C., Gruber A.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Melandris J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

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RA  Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA  Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA  Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA  Setubal J.C., Kitajima J.P.;
RT  "Comparison of the genomes of two Xanthomonas pathogens with differing
RT  host specificities."
RL  Nature 417:459-463(2002).
CC  -1- CATALYTIC ACTIVITY: Protein N(6)-(dihydrolipoyl)lysine + NAD(+) =
CC  protein N(6)-(lipoyl)lysine + NADH.
CC  -1- COFACTOR: Binds 1 FAD per subunit (By similarity).
CC  -1- COFACTOR: FAD (By similarity).
CC  -1- MISCELLANEOUS: The active site is a redox-active disulfide bond
CC  (By similarity).
CC  -1- SIMILARITY: Belongs to the class-I pyridine nucleotide-disulfide
CC  oxidoreductase family.
CC  -1- SIMILARITY: Contains 1 lipoyl-binding domain.
DR  EMBL; AE014016; AAM38502.1; -.
DR  HSSP; Q51245; 1OJT.
DR  GO; GO:0005737; C:cytoplasm; IEA.
DR  GO; GO:0004148; F:dihydrolipoyl dehydrogenase activity; IEA.
DR  GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR  GO; GO:0046872; F:metal ion binding; IEA.
DR  GO; GO:0006118; P:electron transport; IEA.
DR  GO; GO:0006096; P:glycolysis; IEA.
DR  InterPro; IPR000089; Biotin_lipoyl.
DR  InterPro; IPR001327; FAD_pyr_redox.
DR  InterPro; IPR000815; Hg_reductase.
DR  InterPro; IPR011053; Hybrid_motif.
DR  InterPro; IPR006258; Lipamide_dh.
DR  InterPro; IPR003016; Lipoyl_BS.
DR  InterPro; IPR000205; NAD_BS.
DR  InterPro; IPR001100; Pyr_redox.
DR  InterPro; IPR004099; Pyr_redox_dim.
DR  Pfam; PF00364; Biotin_lipoyl; 1.
DR  Pfam; PF00070; Pyr_redox; 1.
DR  Pfam; PF02852; Pyr_redox_dim; 1.
DR  PRINTS; PR00368; FADPNR.
DR  PRINTS; PR00945; HGRDTASE.
DR  PRINTS; PR00411; PNDRDTASEI.
DR  ProDom; PD000139; FAD_pyr_redox; 1.
DR  TIGRFAMs; TIGR01350; Lipamide_DH; 1.
DR  PROSITE; PS00189; LIPOYL; 1.
DR  PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
KW  Complete proteome; FAD; Flavoprotein; lipoyl; NAD; Oxidoreductase;
KW  Redox-active center.
SQ  SEQUENCE 607 AA; 63213 MW; 2D218BCF97903D9F CRC64;

Query Match          53.6%; Score 45; DB 2; Length 607;
Best Local Similarity 64.7%; Pred. No. 73;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  1 APEKAFBAYKAAAPA 17
    |||:| |||||
DB  84 APEKAFKAAAPAAA 100

RESULT 12
Q65JG3 PRELIMINARY; PRT; 781 AA.
ID  Q65JG3;
AC  Q65JG3;
DT  25-OCT-2004 (TREMBlrel. 28, Created)
DT  25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT  25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE  SpoIIE (DNA translocase).
GN  Name=spoIIE; ORFNames=BL01204, BLi01906;
OS  Bacillus licheniformis DSM 13.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=279010;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DSM 13;
RX  PubMed=15383718;
RA  Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,

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RA  Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA  Ehrenreich A., Gottschalk G.;
RT  "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT  Organism with Great Industrial Potential."
RL  J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 14580;
RA  Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA  Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA  Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA  Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA  Berka R.M.;
RT  "Complete genome sequence of the industrial bacterium Bacillus
RT  licheniformis and comparisons with closely related Bacillus species."
RL  Genome Biol. 5:R77-R77(2004).
DR  EMBL; AE017333; AAU40801.1; -.
DR  EMBL; CP000002; AAU23441.1; -.
SQ  SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;

Query Match          53.6%; Score 45; DB 2; Length 781;
Best Local Similarity 60.0%; Pred. No. 93;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  3 EKAKEAYKAAAPA 17
    ||:| |||
DB  264 EKPEVQAYEAPAAPA 278

RESULT 13
Q69YQ8 PRELIMINARY; PRT; 1340 AA.
ID  Q69YQ8;
AC  Q69YQ8;
DT  25-OCT-2004 (TREMBlrel. 28, Created)
DT  25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT  25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE  Hypothetical protein DKFZp451i127 (Fragment).
GN  Name=DKFZp451i127;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Skeletal muscle;
RG  The German cDNA Consortium;
RA  Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA  Fobo G., Han M., Wiemann S.;
RL  Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AL832376; CAH10402.1; -.
KW  Hypothetical protein.
FT  NON_TER 1340 1340
SQ  SEQUENCE 1340 AA; 145772 MW; FA4635B5BE64394 CRC64;

Query Match          53.6%; Score 45; DB 2; Length 1340;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY  3 EKAKEAYKAAAP 16
    |||:| |||||
DB  634 ENBEFAYSPAAAP 647

RESULT 14
Q69YQ9 PRELIMINARY; PRT; 1614 AA.
ID  Q69YQ9;
AC  Q69YQ9;
DT  25-OCT-2004 (TREMBlrel. 28, Created)
DT  25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT  25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE  Hypothetical protein DKFZp451A076 (Fragment).
GN  Name=DKFZp451A076;
OS  Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RG The German cDNA Consortium;  
 RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.,  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL832347; CA10406.1; -.  
 KM Hypothetical protein.  
 FT NON TER 1614 1614  
 SQ SEQUENCE 1614 AA; 175041 MW; FCE219C927BAEB9B CRC64;

Query Match 53.6%; Score 45; DB 2; Length 1614;  
 Best Local Similarity 64.3%; Pred. No. 1.9e+02;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY .3 EKAKFEAYKAAAP 16  
 :|||  
 Db 562 ENEFEAYSPAAAP 575

## RESULT 15

Q98EL9 PRELIMINARY; PRT; 427 AA.  
 AC Q98EL9;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE M11418 protein.  
 GN OrderedLocuNames=m11418;  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003003; BAB50899.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 427 AA; 46687 MW; 8FB54C7A4F6C6676 CRC64;

Query Match 53.0%; Score 44.5; DB 2; Length 427;  
 Best Local Similarity 58.8%; Pred. No. 63;  
 Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 2 PEKAKFEA-YKAAAPA 17  
 :|||  
 Db 173 PQRAAFARYLSASAPA 189

Search completed: February 26, 2005, 23:55:46  
 Job time : 75.898 secs